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OM nucleic - nucleic search, using sw model

Run on: December 3, 2004, 02:05:35 ; Search time 1585.42 seconds  
(without alignments)  
62.385 Million cell updates/sec

Title: US-10-050-189A-9

Perfect score: 18  
Sequence: 1 atgcttggtacttgctg 18

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3694831 seqs, 2747406616 residues

Total number of hits satisfying chosen parameters: 7398662

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published Applications NA:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	US-10-050-189A-9	Sequence 9, Appli
C 2	18	100.0	13	US-10-041-856-1	Sequence 1, Appli
C 3	16.4	91.1	830	US-10-027-632-27387	Sequence 27387, A
C 4	16.4	91.1	830	US-10-027-632-27387	Sequence 27387, A
5	16	88.9	461	US-10-027-632-135313	Sequence 135313, A
6	16	88.9	461	US-10-027-632-135313	Sequence 135313, A
C 7	15.4	85.6	263	US-10-027-632-14998	Sequence 14998, A
C 8	15.4	85.6	343	US-10-027-632-14998	Sequence 14998, A
C 9	15.4	85.6	449	US-10-027-632-14998	Sequence 14998, A
C 10	15.4	85.6	516	US-10-027-632-14998	Sequence 14998, A
C 11	15.4	85.6	516	US-10-027-632-14998	Sequence 14998, A
C 12	15.4	85.6	516	US-10-027-632-14998	Sequence 14998, A

## SUMMARIES

13	15.4	85.6	516	15	US-10-027-632-288642	Sequence 288642, A
C 14	15.4	85.6	630	13	US-10-027-632-274201	Sequence 274201, A
C 15	15.4	85.6	630	13	US-10-027-632-274201	Sequence 274201, A
C 16	15.4	85.6	666	13	US-10-027-632-203435	Sequence 203435, A
C 17	15.4	85.6	666	13	US-10-027-632-203435	Sequence 203435, A
18	15.4	85.6	706	16	US-10-027-632-203435	Sequence 203435, A
19	15.4	85.6	783	17	US-10-027-632-203435	Sequence 203435, A
20	15.4	85.6	1021	16	US-10-027-632-203435	Sequence 203435, A
21	15.4	85.6	1021	16	US-10-027-632-203435	Sequence 203435, A
22	15.4	85.6	1077	18	US-10-027-632-203435	Sequence 203435, A
23	15.4	85.6	1366	16	US-10-027-632-203435	Sequence 203435, A
C 24	15.4	85.6	1441	18	US-10-027-632-203435	Sequence 203435, A
25	15.4	85.6	1489	18	US-10-027-632-203435	Sequence 203435, A
26	15.4	85.6	1507	16	US-10-027-632-203435	Sequence 203435, A
27	15.4	85.6	1536	16	US-10-027-632-203435	Sequence 203435, A
28	15.4	85.6	1852	18	US-10-027-632-203435	Sequence 203435, A
C 29	15.4	85.6	2112	15	US-10-027-632-203435	Sequence 203435, A
30	15.4	85.6	27499	17	US-10-027-632-203435	Sequence 203435, A
31	15.4	85.6	153740	17	US-10-027-632-203435	Sequence 203435, A
32	15.4	85.6	271990	15	US-10-027-632-203435	Sequence 203435, A
33	15.4	85.6	271990	15	US-10-027-632-203435	Sequence 203435, A
C 34	15.4	85.6	744802	15	US-10-027-632-203435	Sequence 203435, A
35	15	83.3	25	13	US-10-027-632-176502	Sequence 176502, A
36	15	83.3	25	13	US-10-027-632-176502	Sequence 176502, A
37	15	83.3	157	16	US-10-027-632-176502	Sequence 176502, A
38	15	83.3	157	16	US-10-027-632-176502	Sequence 176502, A
C 39	15	83.3	873	16	US-10-027-632-176502	Sequence 176502, A
40	15	83.3	1453	16	US-10-027-632-176502	Sequence 176502, A
41	15	83.3	4340	14	US-10-027-632-176502	Sequence 176502, A
42	15	83.3	5170	10	US-10-027-632-176502	Sequence 176502, A
43	14.8	82.2	271	16	US-10-027-632-176502	Sequence 176502, A
44	14.8	82.2	308	17	US-10-027-632-176502	Sequence 176502, A
C 45	14.8	82.2	310	16	US-10-027-632-176502	Sequence 176502, A
C 46	14.8	82.2	310	16	US-10-027-632-176502	Sequence 176502, A
47	14.8	82.2	398	16	US-10-027-632-176502	Sequence 176502, A
48	14.8	82.2	398	16	US-10-027-632-176502	Sequence 176502, A
C 49	14.8	82.2	416	16	US-10-027-632-176502	Sequence 176502, A
50	14.8	82.2	431	13	US-10-027-632-176502	Sequence 176502, A
51	14.8	82.2	431	13	US-10-027-632-176502	Sequence 176502, A
C 52	14.8	82.2	449	15	US-10-027-632-176502	Sequence 176502, A
53	14.8	82.2	451	18	US-10-027-632-176502	Sequence 176502, A
C 54	14.8	82.2	456	16	US-10-027-632-176502	Sequence 176502, A
C 55	14.8	82.2	456	16	US-10-027-632-176502	Sequence 176502, A
56	14.8	82.2	474	16	US-10-027-632-176502	Sequence 176502, A
57	14.8	82.2	516	17	US-10-027-632-176502	Sequence 176502, A
58	14.8	82.2	529	17	US-10-027-632-176502	Sequence 176502, A
59	14.8	82.2	554	9	US-10-027-632-176502	Sequence 176502, A
60	14.8	82.2	554	14	US-10-027-632-176502	Sequence 176502, A
61	14.8	82.2	554	16	US-10-027-632-176502	Sequence 176502, A
62	14.8	82.2	554	17	US-10-027-632-176502	Sequence 176502, A
63	14.8	82.2	554	17	US-10-027-632-176502	Sequence 176502, A
C 64	14.8	82.2	575	15	US-10-027-632-176502	Sequence 176502, A
65	14.8	82.2	585	13	US-10-027-632-176502	Sequence 176502, A
66	14.8	82.2	585	13	US-10-027-632-176502	Sequence 176502, A
67	14.8	82.2	585	15	US-10-027-632-176502	Sequence 176502, A
68	14.8	82.2	585	15	US-10-027-632-176502	Sequence 176502, A
69	14.8	82.2	585	16	US-10-027-632-176502	Sequence 176502, A
70	14.8	82.2	597	14	US-10-027-632-176502	Sequence 176502, A
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72	14.8	82.2	626	18	US-10-027-632-176502	Sequence 176502, A
73	14.8	82.2	855	18	US-10-027-632-176502	Sequence 176502, A
74	14.8	82.2	856	16	US-10-027-632-176502	Sequence 176502, A
75	14.8	82.2	940	13	US-10-027-632-176502	Sequence 176502, A
76	14.8	82.2	940	15	US-10-027-632-176502	Sequence 176502, A
77	14.8	82.2	1156	16	US-10-027-632-176502	Sequence 176502, A
78	14.8	82.2	1194	16	US-10-027-632-176502	Sequence 176502, A
C 79	14.8	82.2	1249	16	US-10-027-632-176502	Sequence 176502, A
C 80	14.8	82.2	1249	16	US-10-027-632-176502	Sequence 176502, A
C 81	14.8	82.2	1351	16	US-10-027-632-176502	Sequence 176502, A
C 82	14.8	82.2	1418	18	US-10-027-632-176502	Sequence 176502, A
C 83	14.8	82.2	1497	18	US-10-027-632-176502	Sequence 176502, A
C 84	14.8	82.2	2079	17	US-10-027-632-176502	Sequence 176502, A
C 85	14.8	82.2	2449	17	US-10-027-632-176502	Sequence 176502, A



C 232	13.8	76.7	233	16	US-10-085-783A-52372	Sequence 53372, A	305	13.8	76.7	583	15	US-10-027-632-282534	Sequence 282534,
C 233	13.8	76.7	237	18	US-10-425-115-5293	Sequence 5293, Ap	C 306	13.8	76.7	588	16	US-10-260-238-5662	Sequence 5662, Ap
C 234	13.8	76.7	255	10	US-09-930-213-433	Sequence 634, App	C 307	13.8	76.7	598	13	US-10-027-633-184666	Sequence 184666,
C 235	13.8	76.7	258	18	US-10-653-047-3559	Sequence 3559, Ap	C 308	13.8	76.7	598	15	US-10-027-633-184666	Sequence 184666,
C 236	13.8	76.7	272	16	US-10-424-599-38327	Sequence 38327, A	C 309	13.8	76.7	602	17	US-10-021-323-1109	Sequence 1109, Ap
C 237	13.8	76.7	276	9	US-09-294-093B-2382	Sequence 2382, Ap	C 310	13.8	76.7	611	13	US-10-027-632-289840	Sequence 289840,
C 238	13.8	76.7	285	18	US-10-425-115-35687	Sequence 35687, A	C 311	13.8	76.7	621	15	US-10-027-633-289840	Sequence 289840,
C 239	13.8	76.7	319	18	US-10-425-115-105151	Sequence 105151,	C 312	13.8	76.7	634	13	US-10-027-633-184048	Sequence 184048,
C 240	13.8	76.7	324	17	US-10-437-963-80882	Sequence 80882, A	C 313	13.8	76.7	634	15	US-10-027-633-184048	Sequence 184048,
C 241	13.8	76.7	325	9	US-09-783-590-10680	Sequence 1660, Ap	C 314	13.8	76.7	631	13	US-10-027-633-185782	Sequence 185782,
C 242	13.8	76.7	325	9	US-09-736-457-269	Sequence 269, App	C 315	13.8	76.7	631	13	US-10-027-633-185783	Sequence 185783,
C 243	13.8	76.7	325	9	US-09-902-941-268	Sequence 268, App	C 316	13.8	76.7	631	15	US-10-027-633-185782	Sequence 185782,
C 244	13.8	76.7	325	9	US-09-849-626-269	Sequence 269, App	C 317	13.8	76.7	631	15	US-10-027-633-185783	Sequence 185783,
C 245	13.8	76.7	325	14	US-09-476-300-269	Sequence 269, App	C 318	13.8	76.7	636	17	US-10-767-701-17036	Sequence 17036, A
C 246	13.8	76.7	325	14	US-10-017-754-269	Sequence 269, App	C 319	13.8	76.7	636	13	US-10-027-633-246986	Sequence 246986,
C 247	13.8	76.7	325	15	US-10-113-872-269	Sequence 269, App	C 320	13.8	76.7	636	15	US-10-027-633-246986	Sequence 246986,
C 248	13.8	76.7	325	15	US-10-283-017-269	Sequence 269, App	C 321	13.8	76.7	636	13	US-10-027-633-141324	Sequence 141324,
C 249	13.8	76.7	346	10	US-09-980-706-281	Sequence 281, App	C 322	13.8	76.7	639	15	US-10-027-633-141324	Sequence 141324,
C 250	13.8	76.7	359	16	US-10-424-599-3456	Sequence 83456, A	C 323	13.8	76.7	646	18	US-10-425-115-137757	Sequence 137757,
C 251	13.8	76.7	362	16	US-10-242-535A-49828	Sequence 49828, A	C 324	13.8	76.7	647	13	US-10-027-632-22240	Sequence 22240, A
C 252	13.8	76.7	362	16	US-10-085-783A-49828	Sequence 49828, A	C 325	13.8	76.7	647	15	US-10-027-632-22240	Sequence 22240, A
C 253	13.8	76.7	364	18	US-10-674-124A-21095	Sequence 21095, A	C 326	13.8	76.7	647	17	US-10-767-701-10697	Sequence 10697, A
C 254	13.8	76.7	375	18	US-10-425-115-14781	Sequence 14781, A	C 327	13.8	76.7	652	17	US-10-437-963-91536	Sequence 91536, A
C 255	13.8	76.7	386	18	US-10-425-115-86435	Sequence 86435, A	C 328	13.8	76.7	660	18	US-10-425-115-137719	Sequence 137719,
C 256	13.8	76.7	400	16	US-10-242-535A-21499	Sequence 21499, A	C 329	13.8	76.7	661	18	US-10-425-115-51449	Sequence 51449, A
C 257	13.8	76.7	400	16	US-10-085-783A-21499	Sequence 21499, A	C 330	13.8	76.7	664	13	US-10-027-632-271384	Sequence 271384,
C 258	13.8	76.7	402	9	US-09-974-300-6934	Sequence 6934, Ap	C 331	13.8	76.7	664	15	US-10-027-632-271384	Sequence 271384,
C 259	13.8	76.7	422	10	US-09-814-353-892	Sequence 892, App	C 332	13.8	76.7	667	17	US-10-437-963-57437	Sequence 57437, A
C 260	13.8	76.7	422	10	US-09-814-353-7263	Sequence 7263, Ap	C 333	13.8	76.7	676	13	US-10-027-632-199183	Sequence 199183,
C 261	13.8	76.7	435	18	US-10-425-115-86436	Sequence 86436, A	C 334	13.8	76.7	676	15	US-10-027-632-199183	Sequence 199183,
C 262	13.8	76.7	438	10	US-09-918-995-10989	Sequence 10989, A	C 335	13.8	76.7	680	13	US-10-027-633-19613	Sequence 19613, A
C 263	13.8	76.7	440	14	US-10-198-846-14036	Sequence 14036, A	C 336	13.8	76.7	680	15	US-10-027-633-19613	Sequence 19613, A
C 264	13.8	76.7	441	16	US-10-062-674-430	Sequence 430, App	C 337	13.8	76.7	683	13	US-10-027-632-255922	Sequence 255922,
C 265	13.8	76.7	451	9	US-09-783-590-1665	Sequence 1665, App	C 338	13.8	76.7	683	15	US-10-027-632-255922	Sequence 255922,
C 266	13.8	76.7	454	16	US-10-424-599-32990	Sequence 32990, A	C 339	13.8	76.7	688	16	US-10-653-047-5330	Sequence 5330, Ap
C 267	13.8	76.7	459	9	US-09-864-761-1379	Sequence 1379, Ap	C 340	13.8	76.7	688	16	US-10-424-599-53366	Sequence 53366, A
C 268	13.8	76.7	459	16	US-10-424-599-62080	Sequence 62080, A	C 341	13.8	76.7	689	13	US-10-767-795-909	Sequence 909, App
C 269	13.8	76.7	460	10	US-09-918-995-99677	Sequence 99677, A	C 342	13.8	76.7	693	13	US-10-027-632-164391	Sequence 164391,
C 270	13.8	76.7	468	16	US-10-242-535A-38518	Sequence 38518, A	C 343	13.8	76.7	693	13	US-10-027-632-164392	Sequence 164392,
C 271	13.8	76.7	468	16	US-10-085-783A-38518	Sequence 38518, A	C 344	13.8	76.7	693	15	US-10-027-632-164391	Sequence 164391,
C 272	13.8	76.7	471	9	US-09-864-761-15197	Sequence 15197, A	C 345	13.8	76.7	693	15	US-10-027-632-164392	Sequence 164392,
C 273	13.8	76.7	475	10	US-09-814-353-13682	Sequence 13682, A	C 346	13.8	76.7	697	13	US-10-027-632-98565	Sequence 98565, A
C 274	13.8	76.7	476	17	US-10-437-963-14855	Sequence 14855, A	C 347	13.8	76.7	697	15	US-10-027-632-98565	Sequence 98565, A
C 275	13.8	76.7	478	18	US-10-425-115-153474	Sequence 153474, A	C 348	13.8	76.7	703	16	US-10-424-599-119224	Sequence 119224,
C 276	13.8	76.7	482	13	US-10-027-632-183087	Sequence 183087, A	C 349	13.8	76.7	710	17	US-10-437-963-96375	Sequence 96375, A
C 277	13.8	76.7	482	13	US-10-027-632-183087	Sequence 183087, A	C 350	13.8	76.7	711	18	US-10-653-047-4548	Sequence 4548, Ap
C 278	13.8	76.7	491	16	US-10-341-961A-94	Sequence 94, Appl	C 351	13.8	76.7	712	13	US-10-027-632-253968	Sequence 253968,
C 279	13.8	76.7	491	16	US-10-341-961A-389	Sequence 389, App	C 352	13.8	76.7	712	13	US-10-027-632-253968	Sequence 253968,
C 280	13.8	76.7	499	10	US-09-918-995-231126	Sequence 231126, A	C 353	13.8	76.7	713	16	US-10-424-599-18240	Sequence 18240, A
C 281	13.8	76.7	500	16	US-10-424-599-331196	Sequence 331196, A	C 354	13.8	76.7	721	13	US-10-027-632-148117	Sequence 148117,
C 282	13.8	76.7	501	17	US-10-437-963-83341	Sequence 83341, A	C 355	13.8	76.7	721	15	US-10-027-632-148117	Sequence 148117,
C 283	13.8	76.7	509	17	US-10-437-963-74199	Sequence 74199, A	C 356	13.8	76.7	721	15	US-10-027-632-24140	Sequence 24140, A
C 284	13.8	76.7	510	10	US-09-814-353-926	Sequence 926, App	C 357	13.8	76.7	736	13	US-10-027-632-24140	Sequence 24140, A
C 285	13.8	76.7	510	10	US-09-814-353-926	Sequence 926, App	C 358	13.8	76.7	736	15	US-10-027-632-24141	Sequence 24141, A
C 286	13.8	76.7	551	9	US-09-815-242-4825	Sequence 4825, Ap	C 359	13.8	76.7	747	17	US-10-437-963-8132	Sequence 8132, Ap
C 287	13.8	76.7	552	9	US-09-864-761-9038	Sequence 9038, Ap	C 360	13.8	76.7	748	16	US-10-424-599-41322	Sequence 41322, A
C 288	13.8	76.7	556	13	US-10-027-632-90704	Sequence 90704, A	C 361	13.8	76.7	748	17	US-10-717-897-31	Sequence 31, Appl
C 289	13.8	76.7	556	13	US-10-027-632-905577	Sequence 905577, A	C 362	13.8	76.7	748	17	US-10-424-599-134874	Sequence 134874,
C 290	13.8	76.7	556	15	US-10-027-632-90704	Sequence 90704, A	C 363	13.8	76.7	760	16	US-10-424-599-230-22	Sequence 22, Appl
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C 292	13.8	76.7	572	13	US-10-027-632-209634	Sequence 209634, A	C 365	13.8	76.7	767	13	US-10-027-632-167635	Sequence 167635,
C 293	13.8	76.7	572	13	US-10-027-632-209634	Sequence 209634, A	C 366	13.8	76.7	767	13	US-10-027-632-167635	Sequence 167635,
C 294	13.8	76.7	573	10	US-09-764-891-7665	Sequence 7665, Ap	C 367	13.8	76.7	767	15	US-10-027-632-167635	Sequence 167635,
C 295	13.8	76.7	575	16	US-10-264-049-1263	Sequence 1263, Ap	C 368	13.8	76.7	767	15	US-10-027-632-167635	Sequence 167635,
C 296	13.8	76.7	578	13	US-10-027-632-61725	Sequence 61725, A	C 369	13.8	76.7	785	17	US-10-437-963-23269	Sequence 23269, A
C 297	13.8	76.7	578	13	US-10-027-632-276042	Sequence 276042, A	C 370	13.8	76.7	797	13	US-10-027-632-138790	Sequence 138790,
C 298	13.8	76.7	578	13	US-10-027-632-276043	Sequence 276043, A	C 371	13.8	76.7	797	13	US-10-027-632-138791	Sequence 138791,
C 299	13.8	76.7	578	13	US-10-027-632-276044	Sequence 276044, A	C 372	13.8	76.7	797	15	US-10-027-632-138790	Sequence 138790,
C 300	13.8	76.7	578	15	US-10-027-632-61725	Sequence 61725, A	C 373	13.8	76.7	797	15	US-10-027-632-138791	Sequence 138791,
C 301	13.8	76.7	578	15	US-10-027-632-276042	Sequence 276042, A	C 374	13.8	76.7	798	13	US-10-027-632-158387	Sequence 158387,
C 302	13.8	76.7	578	15	US-10-027-632-276043	Sequence 276043, A	C 375	13.8	76.7	798	13	US-10-027-632-158387	Sequence 158387,
C 303	13.8	76.7	578	15	US-10-027-632-276044	Sequence 276044, A	C 376	13.8	76.7	804	18	US-10-425-115-29999	Sequence 29999, A
C 304	13.8	76.7	583	13	US-10-027-632-282534	Sequence 282534, A	C 377	13.8	76.7	807	16	US-10-424-599-140327	Sequence 140327,

C 378	13.8	76.7	809	13	US-10-027-632-8114	Sequence 8114, Ap	C 451	13.8	76.7	1857	9	US-09-738-626-1808	Sequence 1808, Ap
C 379	13.8	76.7	809	13	US-10-027-632-9959	Sequence 9959, Ap	C 452	13.8	76.7	2000	16	US-10-260-238-2210	Sequence 2210, Ap
C 380	13.8	76.7	809	15	US-10-027-632-8114	Sequence 8114, Ap	C 453	13.8	76.7	2016	17	US-10-437-963-11556	Sequence 11556, A
C 381	13.8	76.7	809	15	US-10-027-632-9959	Sequence 9959, Ap	C 454	13.8	76.7	2017	17	US-10-437-963-79852	Sequence 79852, A
C 382	13.8	76.7	809	17	US-10-437-963-88527	Sequence 88527, A	C 455	13.8	76.7	2017	17	US-10-437-963-79813	Sequence 79813, A
C 383	13.8	76.7	809	18	US-10-425-115-48365	Sequence 48365, A	C 456	13.8	76.7	2026	13	US-10-027-632-97254	Sequence 97254, A
C 384	13.8	76.7	833	13	US-10-027-632-126773	Sequence 126773, A	C 457	13.8	76.7	2026	13	US-10-027-632-97254	Sequence 97254, A
C 385	13.8	76.7	833	15	US-10-027-632-126773	Sequence 126773, A	C 458	13.8	76.7	2026	15	US-10-027-632-97254	Sequence 97254, A
C 386	13.8	76.7	840	16	US-10-108-260A-1473	Sequence 1473, Ap	C 459	13.8	76.7	2026	15	US-10-027-632-97254	Sequence 97254, A
C 387	13.8	76.7	852	16	US-10-108-260A-1473	Sequence 1473, Ap	C 460	13.8	76.7	2026	15	US-10-027-632-97254	Sequence 97254, A
C 388	13.8	76.7	853	16	US-10-191-803-870	Sequence 870, Ap	C 461	13.8	76.7	2027	15	US-10-027-632-259232	Sequence 259232, A
C 389	13.8	76.7	856	13	US-10-029-630-7	Sequence 7, Appl	C 462	13.8	76.7	2031	16	US-10-027-632-259232	Sequence 259232, A
C 390	13.8	76.7	886	13	US-10-116-278-277	Sequence 277, Appl	C 463	13.8	76.7	2040	13	US-10-027-632-98287	Sequence 98287, A
C 391	13.8	76.7	892	17	US-10-437-963-16791	Sequence 16791, A	C 464	13.8	76.7	2040	15	US-10-027-632-98287	Sequence 98287, A
C 392	13.8	76.7	922	13	US-10-027-632-120074	Sequence 120074, A	C 465	13.8	76.7	2080	18	US-10-425-115-47599	Sequence 47599, A
C 393	13.8	76.7	922	13	US-10-027-632-120075	Sequence 120075, A	C 466	13.8	76.7	2098	9	US-09-917-800A-1707	Sequence 1707, Ap
C 394	13.8	76.7	922	13	US-10-027-632-120075	Sequence 120075, A	C 467	13.8	76.7	2098	16	US-10-152-319A-1800	Sequence 1800, Ap
C 395	13.8	76.7	922	15	US-10-027-632-120075	Sequence 120075, A	C 468	13.8	76.7	2162	16	US-10-424-599-29795	Sequence 29795, A
C 396	13.8	76.7	922	15	US-10-027-632-120075	Sequence 120075, A	C 469	13.8	76.7	2162	17	US-10-437-963-7592	Sequence 7592, Ap
C 397	13.8	76.7	922	15	US-10-027-632-120076	Sequence 120076, A	C 470	13.8	76.7	2244	16	US-10-424-599-37021	Sequence 37021, A
C 398	13.8	76.7	923	16	US-10-264-049-118	Sequence 118, Appl	C 471	13.8	76.7	2254	15	US-10-106-698-249	Sequence 249, Appl
C 399	13.8	76.7	937	14	US-10-013-600B-27	Sequence 27, Appl	C 472	13.8	76.7	2259	10	US-09-948-820-30	Sequence 30, Appl
C 400	13.8	76.7	942	15	US-10-037-270-762	Sequence 762, Appl	C 473	13.8	76.7	2259	18	US-10-613-076-30	Sequence 30, Appl
C 401	13.8	76.7	942	15	US-10-117-722-762	Sequence 762, Appl	C 474	13.8	76.7	2360	16	US-10-398-221-1904	Sequence 1904, Ap
C 402	13.8	76.7	964	17	US-10-437-963-49905	Sequence 49905, A	C 475	13.8	76.7	2361	16	US-10-282-122A-36277	Sequence 36277, A
C 403	13.8	76.7	987	16	US-10-260-238-5392	Sequence 5392, Ap	C 476	13.8	76.7	2395	17	US-10-437-963-74270	Sequence 74270, A
C 404	13.8	76.7	991	14	US-10-178-523-10	Sequence 10, Appl	C 477	13.8	76.7	2448	16	US-10-149-310-193	Sequence 193, Appl
C 405	13.8	76.7	1033	18	US-10-425-115-131992	Sequence 131992, A	C 478	13.8	76.7	2533	17	US-10-437-963-65463	Sequence 65463, A
C 406	13.8	76.7	1056	10	US-09-814-363-13566	Sequence 13566, A	C 479	13.8	76.7	2601	16	US-10-424-599-31866	Sequence 31866, A
C 407	13.8	76.7	1059	18	US-10-425-115-51805	Sequence 51805, A	C 480	13.8	76.7	2779	16	US-10-108-260A-144	Sequence 144, Appl
C 408	13.8	76.7	1101	16	US-10-425-114-29323	Sequence 29323, A	C 481	13.8	76.7	2790	9	US-09-938-842A-698	Sequence 698, Appl
C 409	13.8	76.7	1101	18	US-10-425-115-40396	Sequence 40396, A	C 482	13.8	76.7	2790	11	US-09-938-842A-698	Sequence 698, Appl
C 410	13.8	76.7	1134	16	US-10-424-599-90248	Sequence 90248, A	C 483	13.8	76.7	2857	16	US-10-425-114-13944	Sequence 12944, A
C 411	13.8	76.7	1142	9	US-09-070-927A-414	Sequence 414, Appl	C 484	13.8	76.7	3008	10	US-09-373-658-3	Sequence 3, Appl
C 412	13.8	76.7	1182	16	US-10-424-599-24931	Sequence 24931, A	C 485	13.8	76.7	3037	15	US-09-989-681-3	Sequence 3, Appl
C 413	13.8	76.7	1203	17	US-10-767-701-10434	Sequence 10434, A	C 486	13.8	76.7	3037	15	US-10-380-911-5	Sequence 5, Appl
C 414	13.8	76.7	1225	17	US-10-767-701-10434	Sequence 10434, A	C 487	13.8	76.7	3078	16	US-09-814-353-13625	Sequence 13625, A
C 415	13.8	76.7	1239	18	US-10-425-115-156489	Sequence 156489, A	C 488	13.8	76.7	3165	16	US-10-282-122A-21520	Sequence 21520, A
C 416	13.8	76.7	1290	17	US-10-474-776-78	Sequence 777, Ap	C 489	13.8	76.7	3168	16	US-10-282-122A-21315	Sequence 21315, A
C 417	13.8	76.7	1293	16	US-10-282-122A-21410	Sequence 21410, A	C 490	13.8	76.7	3172	10	US-09-764-891-8499	Sequence 8499, Ap
C 418	13.8	76.7	1298	18	US-10-425-115-98066	Sequence 98066, A	C 491	13.8	76.7	3195	17	US-10-437-963-71062	Sequence 71062, A
C 419	13.8	76.7	1301	16	US-10-425-114-6940	Sequence 6940, Ap	C 492	13.8	76.7	3376	16	US-10-108-260A-1664	Sequence 1664, Ap
C 420	13.8	76.7	1305	17	US-10-437-963-65368	Sequence 65368, A	C 493	13.8	76.7	3390	17	US-10-437-963-25609	Sequence 25609, A
C 421	13.8	76.7	1312	13	US-10-027-632-250311	Sequence 250311, A	C 494	13.8	76.7	3638	9	US-09-918-171A-8	Sequence 8, Appl
C 422	13.8	76.7	1312	13	US-10-027-632-250311	Sequence 250311, A	C 495	13.8	76.7	3638	10	US-09-764-891-10154	Sequence 10154, A
C 423	13.8	76.7	1312	15	US-10-027-632-250311	Sequence 250311, A	C 496	13.8	76.7	3687	17	US-10-437-963-8714	Sequence 8714, Ap
C 424	13.8	76.7	1312	15	US-10-027-632-250311	Sequence 250311, A	C 497	13.8	76.7	3711	17	US-10-283-978A-398	Sequence 398, Appl
C 425	13.8	76.7	1370	18	US-10-487-752-15	Sequence 15, Appl	C 498	13.8	76.7	3715	16	US-10-425-114-28850	Sequence 28850, A
C 426	13.8	76.7	1374	17	US-10-437-963-65229	Sequence 65229, A	C 499	13.8	76.7	3775	16	US-10-398-221-3666	Sequence 3666, Ap
C 427	13.8	76.7	1392	18	US-10-425-115-4474	Sequence 4474, Ap	C 500	13.8	76.7	4280	10	US-09-764-891-10157	Sequence 10157, A
C 428	13.8	76.7	1440	16	US-10-260-238-5554	Sequence 5554, Ap	C 501	13.8	76.7	4796	9	US-09-764-891-1627	Sequence 1627, Ap
C 429	13.8	76.7	1442	16	US-10-424-599-111930	Sequence 111930, A	C 502	13.8	76.7	4796	14	US-10-092-154-1627	Sequence 1627, Ap
C 430	13.8	76.7	1446	18	US-10-425-115-51808	Sequence 51808, A	C 503	13.8	76.7	5173	13	US-10-194-163-1078	Sequence 1078, Ap
C 431	13.8	76.7	1449	9	US-09-764-903-16	Sequence 16, Appl	C 504	13.8	76.7	5193	17	US-10-437-963-18099	Sequence 18099, A
C 432	13.8	76.7	1449	14	US-10-091-391-16	Sequence 16, Appl	C 505	13.8	76.7	6149	9	US-09-764-887-436	Sequence 436, Appl
C 433	13.8	76.7	1451	9	US-09-925-298-126	Sequence 126, Appl	C 506	13.8	76.7	6149	9	US-09-764-887-437	Sequence 437, Appl
C 434	13.8	76.7	1451	14	US-10-102-806-126	Sequence 126, Appl	C 507	13.8	76.7	6149	14	US-10-073-961-437	Sequence 437, Appl
C 435	13.8	76.7	1473	16	US-10-282-122A-18996	Sequence 18996, A	C 508	13.8	76.7	6149	14	US-10-437-963-69717	Sequence 69717, A
C 436	13.8	76.7	1488	16	US-10-425-114-11757	Sequence 11757, A	C 509	13.8	76.7	6157	17	US-10-437-963-69717	Sequence 69717, A
C 437	13.8	76.7	1493	16	US-10-425-114-29305	Sequence 29305, A	C 510	13.8	76.7	6224	16	US-10-600-230-75	Sequence 75, Appl
C 438	13.8	76.7	1497	18	US-10-425-115-54959	Sequence 54959, A	C 511	13.8	76.7	6828	16	US-10-398-221-3813	Sequence 3813, Ap
C 439	13.8	76.7	1506	18	US-10-425-115-471910	Sequence 471910, A	C 512	13.8	76.7	7568	15	US-10-133-937-60	Sequence 60, Appl
C 440	13.8	76.7	1531	17	US-10-467-595-52	Sequence 52, Appl	C 513	13.8	76.7	7568	15	US-10-159-563-60	Sequence 60, Appl
C 441	13.8	76.7	1587	16	US-10-424-599-29792	Sequence 29792, A	C 514	13.8	76.7	7754	16	US-10-264-213-3	Sequence 3, Appl
C 442	13.8	76.7	1605	16	US-10-282-122A-38560	Sequence 38560, A	C 515	13.8	76.7	10434	14	US-10-091-504-1668	Sequence 1668, Ap
C 443	13.8	76.7	1674	16	US-10-425-114-76745	Sequence 76745, A	C 516	13.8	76.7	10434	16	US-10-227-577-1668	Sequence 1668, Ap
C 444	13.8	76.7	1672	17	US-10-767-701-13289	Sequence 13289, A	C 517	13.8	76.7	10434	16	US-10-227-577-1668	Sequence 1668, Ap
C 445	13.8	76.7	1698	10	US-09-764-891-10155	Sequence 10155, A	C 518	13.8	76.7	10445	9	US-09-764-891-6380	Sequence 6380, Ap
C 446	13.8	76.7	1711	18	US-10-425-115-55013	Sequence 55013, A	C 519	13.8	76.7	10519	9	US-09-764-847-1628	Sequence 1628, Ap
C 447	13.8	76.7	1733	14	US-09-764-903-31	Sequence 31, Appl	C 520	13.8	76.7	10519	14	US-10-092-154-1628	Sequence 1628, Ap
C 448	13.8	76.7	1733	14	US-09-764-903-31	Sequence 31, Appl	C 521	13.8	76.7	13123	10	US-09-764-891-7642	Sequence 7642, Ap
C 449	13.8	76.7	1737	17	US-10-437-963-49904	Sequence 49904, A	C 522	13.8	76.7	13337	9	US-09-764-846-312	Sequence 312, Appl
C 450	13.8	76.7	1840	10	US-09-814-353-20268	Sequence 20268, A	C 523	13.8	76.7	13337	9	US-09-764-847-1629	Sequence 1629, Appl



524	13.8	76.7	13337	14	US-10-091-483-312	Sequence 312, App	597	13.8	76.7	694707	16	US-10-398-221-9	Sequence 9, Appli
525	13.8	76.7	13337	14	US-10-092-154-1629	Sequence 129, App	598	13.8	76.7	1163020	16	US-10-398-221-10	Sequence 10, Appl
526	13.8	76.7	13382	17	US-10-741-601-5759	Sequence 5759, App	599	13.8	76.7	1503841	9	US-09-795-668-1	Sequence 1, Appli
527	13.8	76.7	14872	8	US-08-961-527-72	Sequence 72, Appl	600	13.8	76.7	1503841	9	US-09-795-668-1	Sequence 1, Appli
528	13.8	76.7	14872	8	US-10-158-844-72	Sequence 72, Appl	601	13.8	76.7	1503841	9	US-09-946-807-1	Sequence 1, Appli
529	13.8	76.7	19988	16	US-10-672-787-10	Sequence 10, Appl	602	13.8	76.7	2731748	17	US-10-297-465A-1	Sequence 2058, Ap
530	13.8	76.7	24173	10	US-09-764-891-9294	Sequence 9294, Ap	603	13.8	76.7	3309400	16	US-10-398-221-2058	Sequence 1, Appli
531	13.8	76.7	24173	14	US-10-091-572-855	Sequence 855, App	604	13.8	76.7	3309400	16	US-10-398-221-2058	Sequence 1, Appli
532	13.8	76.7	25000	11	US-09-988-007A-215	Sequence 215, App	605	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
533	13.8	76.7	25975	10	US-09-764-891-7643	Sequence 7643, Ap	606	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
534	13.8	76.7	27566	13	US-10-087-192-1480	Sequence 1480, Ap	607	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
535	13.8	76.7	32167	10	US-09-764-891-8197	Sequence 8197, Ap	608	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
536	13.8	76.7	33769	15	US-10-374-979-8	Sequence 8, Appli	609	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
537	13.8	76.7	33769	16	US-10-182-936A-8	Sequence 8, Appli	610	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
538	13.8	76.7	33769	17	US-10-731-739-8	Sequence 8, Appli	611	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
539	13.8	76.7	33769	18	US-10-477-238A-8	Sequence 1030, Ap	612	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
540	13.8	76.7	39768	13	US-10-087-132-1030	Sequence 12, Appl	613	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
541	13.8	76.7	40138	15	US-10-331-061-12	Sequence 12, Appl	614	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
542	13.8	76.7	42772	13	US-10-087-192-1903	Sequence 1903, Ap	615	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
543	13.8	76.7	43419	15	US-10-017-161-1795	Sequence 1795, Ap	616	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
544	13.8	76.7	43419	15	US-10-292-798-1451	Sequence 1451, Ap	617	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
545	13.8	76.7	47448	15	US-10-085-117-145	Sequence 145, App	618	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
546	13.8	76.7	49087	17	US-10-322-656-1	Sequence 1, Appli	619	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
547	13.8	76.7	50000	10	US-09-902-214-6	Sequence 6, Appli	620	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
548	13.8	76.7	52302	11	US-09-997-722-4	Sequence 4, Appli	621	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
549	13.8	76.7	55544	13	US-10-087-192-811	Sequence 811, App	622	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
550	13.8	76.7	55827	9	US-09-813-133A-3	Sequence 3, Appli	623	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
551	13.8	76.7	55827	14	US-10-212-877-3	Sequence 3, Appli	624	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
552	13.8	76.7	59475	17	US-10-322-656-166	Sequence 166, App	625	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
553	13.8	76.7	63000	9	US-09-780-172-18	Sequence 18, Appl	626	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
554	13.8	76.7	64183	18	US-10-684-422-201	Sequence 201, App	627	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
555	13.8	76.7	71108	13	US-10-087-192-1402	Sequence 1402, Ap	628	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
556	13.8	76.7	81210	17	US-10-741-601-5664	Sequence 5664, Ap	629	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
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558	13.8	76.7	84826	15	US-10-292-081A-1	Sequence 1, Appli	631	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
559	13.8	76.7	88624	16	US-10-608-397-1	Sequence 1, Appli	632	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
560	13.8	76.7	94523	15	US-10-034-650-52	Sequence 52, Appl	633	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
561	13.8	76.7	95960	13	US-10-087-192-1384	Sequence 1384, Ap	634	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
562	13.8	76.7	95960	16	US-10-189-267-20	Sequence 20, Appl	635	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
563	13.8	76.7	98686	16	US-10-087-192-1390	Sequence 1390, Ap	636	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
564	13.8	76.7	106315	13	US-10-087-192-1178	Sequence 178, App	637	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
565	13.8	76.7	107280	17	US-10-322-281-155	Sequence 155, App	638	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
566	13.8	76.7	114633	13	US-10-087-192-737	Sequence 727, App	639	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
567	13.8	76.7	116704	13	US-10-087-192-1456	Sequence 1456, Ap	640	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
568	13.8	76.7	119414	13	US-10-087-192-1807	Sequence 1807, Ap	641	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
569	13.8	76.7	124990	18	US-10-684-422-156	Sequence 156, App	642	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
570	13.8	76.7	130427	14	US-10-175-523-87	Sequence 87, Appl	643	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
571	13.8	76.7	133787	17	US-10-322-081B-61	Sequence 61, Appl	644	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
572	13.8	76.7	133787	15	US-10-236-031B-61	Sequence 61, Appl	645	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
573	13.8	76.7	142338	13	US-10-087-192-1504	Sequence 1504, Ap	646	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
574	13.8	76.7	145597	17	US-10-624-149A-2	Sequence 2, Appli	647	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
575	13.8	76.7	156843	13	US-10-087-192-1408	Sequence 1408, Ap	648	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
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577	13.8	76.7	168325	13	US-10-087-192-955	Sequence 955, App	650	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
578	13.8	76.7	168821	13	US-10-087-192-622	Sequence 622, App	651	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
579	13.8	76.7	174448	13	US-10-087-192-148	Sequence 148, App	652	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
580	13.8	76.7	176594	17	US-10-322-281-495	Sequence 495, App	653	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
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582	13.8	76.7	183999	18	US-10-872-113-1	Sequence 1, Appli	655	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
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587	13.8	76.7	203070	13	US-10-087-192-247	Sequence 247, App	660	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
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590	13.8	76.7	234844	13	US-10-087-192-544	Sequence 544, App	663	13.4	74.4	162	18	US-10-425-115-113241	Sequence 113241,
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C 678	13.4	74.4	611	13	US-10-027-632-187946	Sequence 187946, Ap	C 751	13.4	74.4	1572	16	US-10-424-599-36334	Sequence 36334, A
C 679	13.4	74.4	621	13	US-10-027-632-259028	Sequence 259028, Ap	C 752	13.4	74.4	1575	15	US-10-369-493-43763	Sequence 43763, A
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C 682	13.4	74.4	624	16	US-10-425-114-35773	Sequence 35773, A	C 755	13.4	74.4	1651	13	US-10-027-632-249111	Sequence 249111, A
C 683	13.4	74.4	627	13	US-10-074-024-193	Sequence 193, App	C 756	13.4	74.4	1651	13	US-10-027-632-249112	Sequence 249112, A
C 684	13.4	74.4	637	13	US-10-027-632-217176	Sequence 217176, Ap	C 757	13.4	74.4	1651	15	US-10-027-632-249112	Sequence 249112, A
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C 686	13.4	74.4	647	18	US-10-027-632-462	Sequence 462, App	C 759	13.4	74.4	1716	18	US-10-425-115-59230	Sequence 59230, A
C 687	13.4	74.4	675	15	US-10-027-632-29939	Sequence 29939, A	C 760	13.4	74.4	1769	18	US-10-425-115-59229	Sequence 59229, A
C 688	13.4	74.4	687	17	US-10-027-632-29939	Sequence 29939, A	C 761	13.4	74.4	1795	16	US-10-425-115-59229	Sequence 59229, A
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C 696	13.4	74.4	752	13	US-10-027-632-14570	Sequence 14570, A	C 769	13.4	74.4	1976	14	US-10-227-684-33	Sequence 33, Appl
C 697	13.4	74.4	756	16	US-10-027-632-14570	Sequence 14570, A	C 770	13.4	74.4	1976	14	US-10-227-684-33	Sequence 33, Appl
C 698	13.4	74.4	762	13	US-10-027-632-14570	Sequence 14570, A	C 771	13.4	74.4	1976	14	US-10-227-684-33	Sequence 33, Appl
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C 701	13.4	74.4	762	13	US-10-027-632-14570	Sequence 14570, A	C 774	13.4	74.4	1976	14	US-10-227-684-33	Sequence 33, Appl
C 702	13.4	74.4	774	13	US-10-027-632-151004	Sequence 151004, A	C 775	13.4	74.4	1976	14	US-10-227-684-33	Sequence 33, Appl
C 703	13.4	74.4	774	13	US-10-027-632-151004	Sequence 151004, A	C 776	13.4	74.4	1976	14	US-10-227-684-33	Sequence 33, Appl
C 704	13.4	74.4	781	13	US-10-027-632-151004	Sequence 151004, A	C 777	13.4	74.4	1976	14	US-10-227-684-33	Sequence 33, Appl
C 705	13.4	74.4	781	13	US-10-027-632-151004	Sequence 151004, A	C 778	13.4	74.4	1976	14	US-10-227-684-33	Sequence 33, Appl
C 706	13.4	74.4	782	16	US-10-027-632-158386	Sequence 158386, A	C 779	13.4	74.4	1976	14	US-10-227-684-33	Sequence 33, Appl
C 707	13.4	74.4	795	13	US-10-027-632-158383	Sequence 158383, A	C 780	13.4	74.4	1976	14	US-10-227-684-33	Sequence 33, Appl
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C 715	13.4	74.4	858	13	US-10-027-632-166977	Sequence 166977, A	C 788	13.4	74.4	1976	14	US-10-227-684-33	Sequence 33, Appl
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C 723	13.4	74.4	946	16	US-10-424-599-124338	Sequence 124338, A	C 796	13.4	74.4	1976	14	US-10-227-684-33	Sequence 33, Appl
C 724	13.4	74.4	954	14	US-10-424-599-124338	Sequence 124338, A	C 797	13.4	74.4	1976	14	US-10-227-684-33	Sequence 33, Appl
C 725	13.4	74.4	994	18	US-10-424-599-124338	Sequence 124338, A	C 798	13.4	74.4	1976	14	US-10-227-684-33	Sequence 33, Appl
C 726	13.4	74.4	1093	18	US-10-425-115-116770	Sequence 116770, A	C 799	13.4	74.4	1976	14	US-10-227-684-33	Sequence 33, Appl
C 727	13.4	74.4	1122	9	US-09-833-381-2050	Sequence 2050, Ap	C 800	13.4	74.4	1976	14	US-10-227-684-33	Sequence 33, Appl
C 728	13.4	74.4	1132	18	US-10-425-115-59225	Sequence 59225, A	C 801	13.4	74.4	1976	14	US-10-227-684-33	Sequence 33, Appl
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C 730	13.4	74.4	1183	13	US-10-027-632-101147	Sequence 101147, A	C 803	13.4	74.4	1976	14	US-10-227-684-33	Sequence 33, Appl
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C 732	13.4	74.4	1199	16	US-10-425-114-580	Sequence 580, App	C 805	13.4	74.4	1976	14	US-10-227-684-33	Sequence 33, Appl
C 733	13.4	74.4	1242	13	US-10-027-632-123121	Sequence 123121, A	C 806	13.4	74.4	1976	14	US-10-227-684-33	Sequence 33, Appl
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C 735	13.4	74.4	1242	13	US-10-027-632-123122	Sequence 123122, A	C 808	13.4	74.4	1976	14	US-10-227-684-33	Sequence 33, Appl
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830	13.4	74.4	1976	15	US-10-230-024-33	Sequence 33, Appl	Sequence 33, Appl	13.4	74.4	2463	16	US-10-424-599-530869	Sequence 30869, A
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848	13.4	74.4	1976	15	US-10-218-753-33	Sequence 33, Appl	Sequence 33, Appl	13.4	74.4	2802	17	US-10-437-963-72092	Sequence 72092, A
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860	13.4	74.4	1976	15	US-10-219-530-33	Sequence 33, Appl	Sequence 33, Appl	13.4	74.4	3543	10	US-10-027-632-76197	Sequence 76197, A
861	13.4	74.4	1976	15	US-10-219-531-33	Sequence 33, Appl	Sequence 33, Appl	13.4	74.4	3543	10	US-10-027-632-76197	Sequence 76197, A
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863	13.4	74.4	1976	15	US-10-219-533-33	Sequence 33, Appl	Sequence 33, Appl	13.4	74.4	3555	13	US-10-027-632-76197	Sequence 76197, A
864	13.4	74.4	1976	15	US-10-230-437-33	Sequence 33, Appl	Sequence 33, Appl	13.4	74.4	3584	13	US-10-027-632-114708	Sequence 114708,
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866	13.4	74.4	1976	15	US-10-232-228-33	Sequence 33, Appl	Sequence 33, Appl	13.4	74.4	3584	13	US-10-027-632-114708	Sequence 114708,
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871	13.4	74.4	2000	17	US-10-477-369-56	Sequence 56, Appl	Sequence 56, Appl	13.4	74.4	3741	13	US-10-158-646-24	Sequence 24, Appl
872	13.4	74.4	2000	17	US-10-477-369-56	Sequence 56, Appl	Sequence 56, Appl	13.4	74.4	4090	17	US-10-437-963-51235	Sequence 51235, A
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C 967 13.4 74.4 59001 15 US-10-087-192-13
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## ALIGNMENTS

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; Publication No. US20020168656A1
; GENERAL INFORMATION:
; APPLICANT: Rubin, Berish
; TITLE OF INVENTION: Detection of Mutations in a Gene Encoding IKB Kinase-Complex-Asso
; FILE REFERENCE: Rubin 201
; CURRENT APPLICATION NUMBER: US/10/050,189A
; CURRENT FILING DATE: 2002-01-16
; NUMBER OF SEQ ID NOS: 13
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; SEQ ID NO 9
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US-10-050-189A-9
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; Publication No. US20020169299A1
; GENERAL INFORMATION:
; APPLICANT: SLAUGENHAUPT, SUSAN
; APPLICANT: GUSELLA, JAMES F.
; TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL
; FILE REFERENCE: 1829-4004US1
; CURRENT APPLICATION NUMBER: US/10/041,856
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/260,080
; PRIOR FILING DATE: 2001-01-06
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.1
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US-10-041-856-1
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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.123
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
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US-10-027-632-27387
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Db 210 ATGCTTGGTACTTGGCTG 193
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US-10-027-632-27387/c  
; Sequence 27387, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR FILING DATE: 2000-04-20  
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US-10-027-632-27387

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DB 210 ATGCTTGCTACTAGGCTG 193

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US-10-027-632-135313  
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; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR FILING DATE: 2000-04-20  
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; PRIOR FILING DATE: 1999-08-09  
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## US-10-027-632-135313

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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 87 ATGCTTGCTACTGGC 102

## RESULT 6

US-10-027-632-135313  
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; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR FILING DATE: 1999-08-09  
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; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 135313  
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; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-135313

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DB 87 ATGCTTGCTACTGGC 102

## RESULT 7

US-10-437-963-14998/c  
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; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
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US-10-437-963-14998

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; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 104545
; LENGTH: 343
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; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_26848C.1
US-10-425-115-104545

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; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 51158
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(449)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_146653C.1

US-10-425-115-51158

Query Match      85.6%; Score 15.4; DB 18; Length 449;
Best Local Similarity 94.1%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCCTTGCTACTTGCTG 18
Db 351 TGCCTTGCTACTTGCTG 335

RESULT 10
US-10-027-632-288641
; Sequence 288641, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 288641
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Human
; OTHER INFORMATION:
US-10-027-632-288641

Query Match      85.6%; Score 15.4; DB 13; Length 516;
Best Local Similarity 94.1%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTTGCT 17
Db 294 ATCCTTGCTACTTGCT 310

RESULT 11
US-10-027-632-288642
; Sequence 288642, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
```

```
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 288642
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-288642

Query Match      85.6%; Score 15.4; DB 13; Length 516;
Best Local Similarity 94.1%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTGGCT 17
   |||||
Db 294 ATCCTTGCTACTGGCT 310

RESULT 12
US-10-027-632-288641
; Sequence 288641, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 288641
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-288641

Query Match      85.6%; Score 15.4; DB 15; Length 516;
Best Local Similarity 94.1%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTGGCT 17
   |||||
Db 294 ATCCTTGCTACTGGCT 310

RESULT 13
US-10-027-632-288642
; Sequence 288642, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
```

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; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 288642
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-288642

Query Match      85.6%; Score 15.4; DB 15; Length 516;
Best Local Similarity 94.1%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTGGCT 17
   |||||
Db 294 ATCCTTGCTACTGGCT 310

RESULT 14
US-10-027-632-274201/c
; Sequence 274201, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 274201
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-274201

Query Match      85.6%; Score 15.4; DB 13; Length 630;
Best Local Similarity 94.1%; Pred. No. 5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCTTGCTACTGGCTG 18
   |||||
Db 587 TACTTGCTACTGGCTG 571
```



RESULT 15  
US-10-027-632-274201/c  
; Sequence 274201, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 274201  
; LENGTH: 630  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-274201

Query Match 85.6%; Score 15.4; DB 15; Length 630;  
Best Local Similarity 94.1%; Pred. No. 5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCTTGCTACTTGCTG 18  
| | | | | | | | | | | | | | | | | | | |  
Db 587 TACTTGCTACTTGCTG 571

RESULT 16  
US-10-027-632-203435/c  
; Sequence 203435, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 203435  
; LENGTH: 666

; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-203435

Query Match 85.6%; Score 15.4; DB 13; Length 666;  
Best Local Similarity 94.1%; Pred. No. 5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCTTGCTACTTGCTG 18  
| | | | | | | | | | | | | | | | | | | |  
Db 252 TACTTGCTACTTGCTG 236

RESULT 17  
US-10-027-632-203435/c  
; Sequence 203435, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 203435  
; LENGTH: 666  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-203435

Query Match 85.6%; Score 15.4; DB 15; Length 666;  
Best Local Similarity 94.1%; Pred. No. 5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCTTGCTACTTGCTG 18  
| | | | | | | | | | | | | | | | | | | |  
Db 252 TACTTGCTACTTGCTG 236

RESULT 18  
US-10-425-114-12518  
; Sequence 12518, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Gao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 12518

; LENGTH: 706  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 701181044\_FLI  
US-10-425-114-12518

Query Match 85.6%; Score 15.4; DB 16; Length 706;  
Best Local Similarity 94.1%; Pred. No. 5e+02; 1; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCTTGGTACTGGCTG 18  
|||||  
DB 428 TGCTTGGTACTGGCTG 444

## RESULT 19

US-10-437-963-16789  
; Sequence 16789, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 16789  
; LENGTH: 783  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_22504C.1  
US-10-437-963-16789

Query Match 85.6%; Score 15.4; DB 17; Length 783;  
Best Local Similarity 94.1%; Pred. No. 5e+02; 1; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCTTGGTACTGGCTG 18  
|||||  
DB 336 TGCTTGGTACTGGCTG 352

## RESULT 20

US-10-767-701-12325  
; Sequence 12325, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53535)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 12325  
; LENGTH: 969  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS55321\_1  
US-10-767-701-12325

Query Match 85.6%; Score 15.4; DB 17; Length 969;  
Best Local Similarity 94.1%; Pred. No. 5.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCTTGGTACTGGCTG 18  
|||||  
DB 236 TGCTTGGTACTGGCTG 252

## RESULT 21

US-10-424-599-2724  
; Sequence 2724, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 2724  
; LENGTH: 1021  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_102465C.1  
US-10-424-599-2724

Query Match 85.6%; Score 15.4; DB 16; Length 1021;  
Best Local Similarity 94.1%; Pred. No. 5.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGGTACTGGCT 17  
|||||  
DB 587 ATGCTTGGTACTGGCT 603

## RESULT 22

US-10-474-792-455  
; Sequence 455, Application US/10474792  
; Publication No. US20040236072A1  
; GENERAL INFORMATION:  
; APPLICANT: Olmsted, Stephen  
; APPLICANT: Zagursky, Robert  
; APPLICANT: Nickbarg, Elliot  
; APPLICANT: Winter, Lourie  
; TITLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES  
; FILE REFERENCE: AM 100399  
; CURRENT APPLICATION NUMBER: US/10/474,792  
; CURRENT FILING DATE: 2003-10-14  
; NUMBER OF SEQ ID NOS: 674  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 455  
; LENGTH: 1077  
; TYPE: DNA  
; ORGANISM: Streptococcus pyogenes  
US-10-474-792-455

Query Match 85.6%; Score 15.4; DB 18; Length 1077;  
Best Local Similarity 94.1%; Pred. No. 5.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCTTGGTACTGGCTG 18  
|||||  
DB 908 TGCTAGGTACTGGCTG 924

## RESULT 23

```
US-10-425-114-2795
; Sequence 2795, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 2795
; LENGTH: 1366
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700223971_FLI
US-10-425-114-2795

Query Match      85.6%; Score 15.4; DB 16; Length 1366;
Best Local Similarity 94.1%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 TGCTTGGTACTTGGCTG 18
Db      764 TGCATGGTACTTGGCTG 780

RESULT 24
US-10-425-115-64396/c
; Sequence 64396, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 64396
; LENGTH: 1441
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MR*4577_15872C.1
US-10-425-115-64396

Query Match      85.6%; Score 15.4; DB 18; Length 1441;
Best Local Similarity 94.1%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 TGCTTGGTACTTGGCTG 18
Db      1226 TGCCTGGTACTTGGCTG 1210

RESULT 25
US-10-425-115-18978
; Sequence 18978, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 18978
; LENGTH: 1489
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MR*4577_117309C.1
US-10-425-115-18978

Query Match      85.6%; Score 15.4; DB 18; Length 1489;
Best Local Similarity 94.1%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 TGCTTGGTACTTGGCTG 18
Db      887 TGCATGGTACTTGGCTG 903

RESULT 26
US-10-425-114-25874
; Sequence 25874, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 25874
; LENGTH: 1507
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3960-021-C1_FLI
US-10-425-114-25874

Query Match      85.6%; Score 15.4; DB 16; Length 1507;
Best Local Similarity 94.1%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 TGCTTGGTACTTGGCTG 18
Db      872 TGCATGGTACTTGGCTG 888

RESULT 27
US-10-425-114-6545
; Sequence 6545, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
```

```
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 6545
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700570906_FLI
US-10-425-114-6545

Query Match      85.6%; Score 15.4; DB 16; Length 1536;
Best Local Similarity 94.1%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2   TGCTTGGTACTTGGCTG 18
        ||| ||||| ||||| |||||
Db       934 TGCATGGTACTTGGCTG 950
        .

RESULT 28
US-10-425-115-18977
; Sequence 18977, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 18977
; LENGTH: 1852
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_117308C.1
US-10-425-115-18977

Query Match      85.6%; Score 15.4; DB 18; Length 1852;
Best Local Similarity 94.1%; Pred. No. 5.3e-02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2   TGCTTGGTACTTGGCTG 18
        ||| ||||| ||||| |||||
Db       1013 TGCATGGTACTTGGCTG 1029
        .

RESULT 29
US-10-369-493-46122/c
; Sequence 46122, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkie, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 46122
; LENGTH: 2112
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
```



```
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (408660)..(409123)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (409204)..(409669)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (428381)..(428396)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (472204)..(472330)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (714252)..(714355)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (714447)..(714529)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (739794)..(739891)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (744484)..(744602)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (51812)..(51911)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (57122)..(57221)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (79368)..(79467)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (293951)..(294050)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (310089)..(310188)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (332935)..(332935)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (332992)..(332992)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (362002)..(362101)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (639781)..(639880)
; OTHER INFORMATION: a, t, c, g, unknown or other
; US-10-292-798-1369
```

```
Query Match      85.6%; Score 15.4; DB 15; Length 744802;
Best Local Similarity 94.1%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 TGCTTGACTTGGCTG 18
          |||||
Db      435754 TGCTGGACTTGGCTG 435738
```

```
RESULT 35
US-10-027-632-176502
```

```
; Sequence 176502, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176502
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-176502
```

```
Query Match      83.3%; Score 15; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 GCTTGGTACTTGGCT 17
          |||||
Db      5 GCTTGGTACTTGGCT 19
```

```
RESULT 36
US-10-027-632-176502
; Sequence 176502, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176502
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-176502
```

Query Match 83.3%; Score 15; DB 15; Length 25;  
Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCTTGGTACTTGGCT 17

Db 5 GCTTGGTACTTGGCT 19

## RESULT 37

US-10-242-535A-2393  
; Sequence 2393, Application US/10242535A  
; Publication No. US20040013663A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; APPLICANT: Liew, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US/10/242,535A  
; PRIOR FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: US 10/085,783  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 2393  
; LENGTH: 157  
; TYPE: DNA  
; ORGANISM: Human  
US-10-242-535A-2393

Query Match 83.3%; Score 15; DB 16; Length 157;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTTGGTACTTGG 15

Db 81 ATGCTTGGTACTTGG 95

## RESULT 38

US-10-085-783A-2393  
; Sequence 2393, Application US/10085783A  
; Publication No. US20040037841A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; APPLICANT: Liew, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2002  
; CURRENT APPLICATION NUMBER: US/10/085,783A  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 2393  
; LENGTH: 157  
; TYPE: DNA  
; ORGANISM: Human  
US-10-085-783A-2393

Query Match 83.3%; Score 15; DB 16; Length 157;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTTGGTACTTGG 15  
Db 81 ATGCTTGGTACTTGG 95

## RESULT 39

US-10-282-122A-36064/c  
; Sequence 36064, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 36064  
; LENGTH: 873  
; TYPE: DNA  
; ORGANISM: Streptococcus mutans  
US-10-282-122A-36064

Query Match 83.3%; Score 15; DB 16; Length 873;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CTCTGGTACTTGGCTG 18

Db 501 CTCTGGTACTTGGCTG 487

## RESULT 40

US-10-424-599-107262  
; Sequence 107262, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J  
; APPLICANT: Kovalic, David K  
; APPLICANT: Zhou, Yihua



APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 107262  
; LENGTH: 1453  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_67873C.1  
US-10-424-599-107262

Query Match 83.3%; Score 15; DB 16; Length 1453;  
Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGCTTGGTACTTGGC 16  
|||  
DB 126 TGCTTGGTACTTGGC 140  
|||

RESULT 41  
US-10-198-846-12986  
; Sequence 12986, Application US/10198846  
; Publication No. US2003099974A1  
; GENERAL INFORMATION:  
; APPLICANT: Lillie, James  
; APPLICANT: Xu, Yongyao  
; APPLICANT: Wang, Youzhen  
; APPLICANT: Steinmann, Kathleen  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; TITLE OF INVENTION: THERAPY OF BREAST CANCER  
; FILE REFERENCE: MRI-C49  
; CURRENT APPLICATION NUMBER: US/10/198,846  
; CURRENT FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/306,220  
; PRIOR FILING DATE: 2001-07-18  
; NUMBER OF SEQ ID NOS: 14084  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12986  
; LENGTH: 4340  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1, 4336, 4337, 4338, 4339, 4340  
; OTHER INFORMATION: n = A,T,C or G  
US-10-198-846-12986

Query Match 83.3%; Score 15; DB 14; Length 4340;  
Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGCTTGGTACTTGGC 16  
|||  
DB 3098 TGCTTGGTACTTGGC 3112  
|||

RESULT 42  
US-09-814-353-19563  
; Sequence 19563, Application US/09814353  
; Publication No. US2003016581A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, John  
; APPLICANT: Thompson, Pamela  
; APPLICANT: Lillie, James  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

FILE REFERENCE: MRI-006B  
; CURRENT APPLICATION NUMBER: US/09/814,353  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: US 60/191,031  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/207,124  
; PRIOR FILING DATE: 2000-05-25  
; PRIOR APPLICATION NUMBER: US 60/211,940  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: US 60/216,820  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: US 60/220,661  
; PRIOR FILING DATE: 2000-07-25  
; PRIOR APPLICATION NUMBER: US 60/257,672  
; PRIOR FILING DATE: 2000-12-21  
; NUMBER OF SEQ ID NOS: 22037  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19563  
; LENGTH: 5170  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 106, 5168, 5169, 5170  
; OTHER INFORMATION: n = A,T,C or G  
US-09-814-353-19563

Query Match 83.3%; Score 15; DB 10; Length 5170;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGCTTGGTACTTGGC 16  
|||  
DB 2630 TGCTTGGTACTTGGC 2644  
|||

RESULT 43  
US-10-424-599-116143  
; Sequence 116143, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J  
; APPLICANT: Kovalic, David K  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 116143  
; LENGTH: 271  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(271)  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_75888C.1  
US-10-424-599-116143

Query Match 82.2%; Score 14.8; DB 16; Length 271;  
Best Local Similarity 88.9%; Pred. No. 9.6e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCTTGGTACTTGGCTG 18  
|||  
DB 173 ATACTTGGTACTTGGCAG 190  
|||

RESULT 44

US-10-437-963-74671  
; Sequence 74671, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovacic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 74671  
; LENGTH: 308  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_74834C.1  
US-10-437-963-74671

Query Match 82.2%; Score 14.8; DB 17; Length 308;  
Best Local Similarity 88.9%; Pred. No. 9.6e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGCTTGGTACTTGGCTG 18  
|||||  
Db 271 ATGCTTGGAACTTGCCTG 288

RESULT 45  
US-10-242-535A-5572/c  
; Sequence 5572, Application US/10242535A  
; Publication No. US20040013663A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; APPLICANT: Liew, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US/10/242,535A  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: US 10/085,783  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5572  
; LENGTH: 310  
; TYPE: DNA  
; ORGANISM: Human  
US-10-242-535A-5572

Query Match 82.2%; Score 14.8; DB 16; Length 310;  
Best Local Similarity 88.9%; Pred. No. 9.6e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGCTTGGTACTTGGCTG 18  
|||||  
Db 71 AGCCTTGGTCTTGGCTG 54

RESULT 46  
US-10-085-783A-5572/c

; Sequence 5572, Application US/10085783A  
; Publication No. US20040037841A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; APPLICANT: Liew, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2002  
; CURRENT APPLICATION NUMBER: US/10/085,783A  
; CURRENT FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5572  
; LENGTH: 310  
; TYPE: DNA  
; ORGANISM: Human  
US-10-085-783A-5572

Query Match 82.2%; Score 14.8; DB 16; Length 310;  
Best Local Similarity 88.9%; Pred. No. 9.6e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGCTTGGTACTTGGCTG 18  
|||||  
Db 71 AGCCTTGGTCTTGGCTG 54

RESULT 47  
US-10-242-535A-6104  
; Sequence 6104, Application US/10242535A  
; Publication No. US20040013663A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; APPLICANT: Liew, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US/10/242,535A  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: US 10/085,783  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6104  
; LENGTH: 398  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2)..(2)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (18)..(18)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (38)..(38)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (308)..(308)  
; OTHER INFORMATION: n is a, c, g, or t

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US-10-242-535A-6104
Query Match      82.2%; Score 14.8; DB 16; Length 398;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCTGGTACTTGGCTG 18
    ||||| ||||| ||||| |||||
Db 278 ATGCTGGTCTTGGCTG 295

RESULT 48
US-10-085-783A-6104
; Sequence 6104, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 36994
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 6104
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)..(18)
; OTHER INFORMATION: n is a, c, g, or t
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-6104

Query Match      82.2%; Score 14.8; DB 16; Length 398;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCTGGTACTTGGCTG 18
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Db 278 ATGCTGGTCTTGGCTG 295

RESULT 49
US-10-425-115-120985/c
; Sequence 120985, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
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US-10-425-115-120985
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 120985
; LENGTH: 416
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_41819C.1
US-10-425-115-120985

Query Match      82.2%; Score 14.8; DB 18; Length 416;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCTTGGTACTTGGCTG 18
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Db 306 ATGCATGGTCTTGGCTG 289

RESULT 50
US-10-027-632-42794
; Sequence 42794, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42794
; LENGTH: 431
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-42794

Query Match      82.2%; Score 14.8; DB 13; Length 431;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCTTGGTACTTGGCTG 18
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Db 198 ATGCATGGTCTTGGCTG 215

Search completed: December 3, 2004, 07:44:01
JOB time : 1620.42 secs
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2004, 01:45:05 ; Search time 59.6842 Seconds  
(without alignment)  
214.365 Million cell updates/sec

Title: US-10-050-189A-9

Perfect score: 18  
Sequence: 1 atgtcttgtaactggctg 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued Patents NA:\*  
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2: /cgn2\_6/prodata/1/ina/5B COMB.seq.\*  
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4: /cgn2\_6/prodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/prodata/1/ina/6CTUS COMB.seq.\*  
6: /cgn2\_6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	14.8	82.2	130	4	US-09-370-767-31007
3	14.8	82.2	132	4	US-09-489-039A-3174
4	14.8	82.2	597	4	US-09-669-751-67
5	14.8	82.2	1116	3	US-09-134-001C-307
6	14.8	82.2	1242	4	US-09-543-681A-1863
7	14.8	82.2	1467	4	US-09-976-594-515
8	14.8	82.2	2094	4	US-09-540-236-1681
9	14.8	82.2	2138	4	US-09-270-767-14769
10	14.8	82.2	119211	4	US-09-556-002-40
11	14.4	80.0	499	4	US-09-270-767-3838
12	14.4	80.0	499	4	US-09-270-767-19120
13	14.4	80.0	831	4	US-09-540-236-444
14	14.4	80.0	1750	4	US-09-270-767-11600
15	14.4	80.0	1875	4	US-09-614-221A-385
16	14.4	80.0	2496	4	US-09-799-451-872
17	14.4	80.0	3834	4	US-09-614-221A-353
18	14.4	80.0	5580	4	US-09-614-221A-536
19	14.4	80.0	58909	4	US-09-596-002-30
20	14	77.8	24	4	US-09-388-743-28
21	14	77.8	24	4	US-10-044-543-28
22	14	77.8	573	4	US-09-614-221A-489
23	14	77.8	678	4	US-09-270-767-10413
24	14	77.8	1935	3	US-08-581-148C-13
25	14	77.8	2418	4	US-09-388-743-25
26	14	77.8	2418	4	US-10-044-543-25
27	13.8	76.7	63	1	US-07-627-323B-7

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1	63	76.7	13.8	US-07-627-323-7	Sequence 7, Appli
1	105	76.7	13.8	US-07-627-323B-11	Sequence 11, Appli
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183	183	76.7	13.8	US-09-134-000C-405	Sequence 405, App
256	256	76.7	13.8	US-09-360-376-26	Sequence 26, Appli
259	259	76.7	13.8	US-09-360-376-24	Sequence 24, Appli
262	262	76.7	13.8	US-09-360-376-25	Sequence 25, Appli
267	267	76.7	13.8	US-09-360-376-18	Sequence 18, Appli
274	274	76.7	13.8	US-09-313-294A-1839	Sequence 1839, Ap
281	281	76.7	13.8	US-09-360-376-31	Sequence 31, Appli
289	289	76.7	13.8	US-09-360-376-27	Sequence 27, Appli
291	291	76.7	13.8	US-09-313-294A-6051	Sequence 6051, Ap
297	297	76.7	13.8	US-09-360-376-29	Sequence 29, Appl
325	325	76.7	13.8	US-09-702-705-269	Sequence 269, App
325	325	76.7	13.8	US-09-736-457-269	Sequence 269, App
325	325	76.7	13.8	US-09-614-124B-269	Sequence 269, App
325	325	76.7	13.8	US-09-671-325-269	Sequence 269, App
325	325	76.7	13.8	US-09-589-184-269	Sequence 269, App
345	345	76.7	13.8	US-09-658-824-269	Sequence 269, App
436	436	76.7	13.8	US-09-360-376-34	Sequence 34, Appl
477	477	76.7	13.8	US-09-621-976-18061	Sequence 18061, A
491	491	76.7	13.8	US-09-513-999C-698	Sequence 698, App
497	497	76.7	13.8	US-09-621-976-1044	Sequence 3044, Ap
525	525	76.7	13.8	US-09-513-999C-3893	Sequence 3893, Ap
582	582	76.7	13.8	US-09-621-976-3756	Sequence 3756, Ap
669	669	76.7	13.8	US-09-252-991A-5141	Sequence 5141, Ap
729	729	76.7	13.8	US-09-252-991A-5044	Sequence 5044, Ap
774	774	76.7	13.8	US-09-252-991A-5169	Sequence 5169, Ap
861	861	76.7	13.8	US-09-673-763-5	Sequence 5, Appli
942	942	76.7	13.8	US-09-360-376-9	Sequence 9, Appli
1038	1038	76.7	13.8	US-09-620-312D-762	Sequence 762, App
1038	1038	76.7	13.8	US-09-328-352-2531	Sequence 2531, Ap
1224	1224	76.7	13.8	US-09-107-532A-2163	Sequence 2163, Ap
1260	1260	76.7	13.8	US-09-270-767-13838	Sequence 13838, A
1389	1389	76.7	13.8	US-09-583-110-2466	Sequence 2466, Ap
1389	1389	76.7	13.8	US-09-122-315C-9	Sequence 9, Appli
1512	1512	76.7	13.8	US-09-360-376-9	Sequence 9, Appli
2030	2030	76.7	13.8	US-09-270-767-10328	Sequence 10328, A
2515	2515	76.7	13.8	US-08-705-937-7	Sequence 7, Appli
3126	3126	76.7	13.8	US-08-695-866-1	Sequence 1, Appli
3213	3213	76.7	13.8	US-09-382-184-7	Sequence 7, Appli
3638	3638	76.7	13.8	US-09-369-364A-8	Sequence 8, Appli
5173	5173	76.7	13.8	US-09-221-017B-1078	Sequence 1078, Ap
7754	7754	76.7	13.8	US-09-634-238-3	Sequence 3, Appli
14872	14872	76.7	13.8	US-08-961-527-72	Sequence 72, Appl
19988	19988	76.7	13.8	US-09-596-002-10	Sequence 10, Appl
33769	33769	76.7	13.8	US-09-544-398B-8	Sequence 8, Appli
40138	40138	76.7	13.8	US-09-543-771-8	Sequence 8, Appli
40138	40138	76.7	13.8	US-09-090-793-12	Sequence 12, Appl
5827	5827	76.7	13.8	US-09-231-859-12	Sequence 12, Appl
63000	63000	76.7	13.8	US-09-813-133A-3	Sequence 3, Appli
72928	72928	76.7	13.8	US-09-780-172-18	Sequence 18, Appli
158	158	74.4	13.4	US-09-009-913-1	Sequence 1, Appli
203	203	74.4	13.4	US-08-905-223-159	Sequence 159, App
230	230	74.4	13.4	US-09-513-999C-12252	Sequence 12252, A
326	326	74.4	13.4	US-09-513-999C-34045	Sequence 34045, A
446	446	74.4	13.4	US-09-513-999C-619	Sequence 619, App
541	541	74.4	13.4	US-09-621-976-14288	Sequence 14288, A
783	783	74.4	13.4	US-08-680-506-9	Sequence 9, Appli
937	937	74.4	13.4	US-09-270-767-14391	Sequence 14391, A
954	954	74.4	13.4	US-09-270-767-27340	Sequence 27340, A
1347	1347	74.4	13.4	US-08-927-219-48	Sequence 48, Appl
1452	1452	74.4	13.4	US-08-680-506-5	Sequence 5, Appli
1587	1587	74.4	13.4	US-08-680-506-8	Sequence 8, Appli
1665	1665	74.4	13.4	US-09-248-786A-4120	Sequence 4120, Ap
2233	2233	74.4	13.4	US-08-680-506-6	Sequence 6, Appli
2305	2305	74.4	13.4	US-09-270-767-11716	Sequence 11716, A
5027	5027	74.4	13.4	US-08-680-506-4	Sequence 4, Appli
7479	7479	74.4	13.4	US-09-620-312D-45	Sequence 45, Appli
		74.4	13.4	US-08-680-506-2	Sequence 2, Appli
		74.4	13.4	US-09-991-258-2	Sequence 2, Appli

C 101	13.4	74.4	8321	3	US-08-680-506-1	Sequence 1, Appli	C 174	13.2	73.3	1480	3	US-08-959-524-11	Sequence 11, Appl
C 102	13.4	74.4	9103	1	US-08-466-033-182	Sequence 182, App	C 175	13.2	73.3	1480	4	US-09-611-452A-11	Sequence 11, Appl
C 103	13.4	74.4	9103	1	US-08-444-733-182	Sequence 182, App	C 176	13.2	73.3	1485	3	US-09-372-422A-39	Sequence 39, Appl
C 104	13.4	74.4	9103	2	US-08-464-134-182	Sequence 182, App	C 177	13.2	73.3	1496	1	US-10-140-002-287	Sequence 287, App
C 105	13.4	74.4	9103	2	US-08-461-361-182	Sequence 182, App	C 178	13.2	73.3	1498	1	US-08-321-162-1	Sequence 1, Appl
C 106	13.4	74.4	9103	2	US-08-485-910-182	Sequence 182, App	C 179	13.2	73.3	1498	1	US-08-441-216-1	Sequence 1, Appl
C 107	13.4	74.4	9103	5	PCT-US95-06266-156	Sequence 156, App	C 180	13.2	73.3	1524	4	US-09-328-352-165	Sequence 165, App
C 108	13.4	74.4	10014	3	US-08-927-219-130	Sequence 130, App	C 181	13.2	73.3	1547	4	US-09-558-002-16	Sequence 16, Appl
C 109	13.4	74.4	11459	3	US-08-454-721A-3	Sequence 3, Appli	C 182	13.2	73.3	1557	3	US-09-919-039-161	Sequence 161, App
C 110	13.4	74.4	12379	4	US-08-991-258-14	Sequence 14, Appl	C 183	13.2	73.3	1565	3	US-08-468-846-1	Sequence 1, Appl
C 111	13.4	74.4	12523	4	US-08-991-258-1	Sequence 1, Appli	C 184	13.2	73.3	1565	3	US-08-915-096A-1	Sequence 1, Appl
C 112	13.4	74.4	13584	4	US-09-991-258-17	Sequence 17, Appl	C 185	13.2	73.3	1605	3	US-09-252-991A-14154	Sequence 14154, A
C 113	13.4	74.4	17056	3	US-09-245-041-3	Sequence 3, Appli	C 186	13.2	73.3	1617	2	US-08-967-508-18	Sequence 18, Appl
C 114	13.4	74.4	17056	4	US-09-358-055B-3	Sequence 3, Appli	C 187	13.2	73.3	1617	2	US-08-967-506-18	Sequence 18, Appl
C 115	13.4	74.4	17056	4	US-08-893-238-3	Sequence 3, Appli	C 188	13.2	73.3	1617	5	PCT-US94-02552-18	Sequence 18, Appl
C 116	13.2	73.3	109	4	US-09-513-999C-14549	Sequence 14549, A	C 189	13.2	73.3	1665	4	US-09-248-786A-3125	Sequence 3125, Ap
C 117	13.2	73.3	117	4	US-08-493-795B-345	Sequence 345, App	C 190	13.2	73.3	1680	2	US-08-967-506-11	Sequence 11, Appl
C 118	13.2	73.3	126	4	US-08-493-795B-343	Sequence 343, App	C 191	13.2	73.3	1680	3	PCT-US94-02552-11	Sequence 11, Appl
C 119	13.2	73.3	154	4	US-08-493-795B-323	Sequence 323, App	C 192	13.2	73.3	1680	5	PCT-US94-02552-11	Sequence 11, Appl
C 120	13.2	73.3	156	4	US-09-513-999C-21821	Sequence 21821, A	C 193	13.2	73.3	1716	4	US-09-134-000C-1963	Sequence 1963, Ap
C 121	13.2	73.3	181	4	US-09-513-999C-20387	Sequence 20387, A	C 194	13.2	73.3	1720	4	US-08-823-038A-41	Sequence 41, Appl
C 122	13.2	73.3	219	4	US-08-493-795B-84	Sequence 84, Appl	C 195	13.2	73.3	1759	1	US-08-726-525-5	Sequence 5, Appli
C 123	13.2	73.3	227	4	US-08-493-795B-76	Sequence 76, Appl	C 196	13.2	73.3	1759	1	US-08-487-942-5	Sequence 5, Appli
C 124	13.2	73.3	265	4	US-08-513-999C-31777	Sequence 31777, A	C 197	13.2	73.3	1759	2	US-08-726-036A-5	Sequence 5, Appli
C 125	13.2	73.3	310	4	US-09-513-999C-1196	Sequence 1196, Ap	C 198	13.2	73.3	1759	3	US-08-083-516-5	Sequence 5, Appli
C 126	13.2	73.3	322	4	US-08-854-133-555	Sequence 555, App	C 199	13.2	73.3	1824	4	US-09-252-991A-14243	Sequence 14243, A
C 127	13.2	73.3	331	3	US-08-651-155B-223	Sequence 223, App	C 200	13.2	73.3	1834	4	US-09-248-796A-6659	Sequence 6659, Ap
C 128	13.2	73.3	331	4	US-09-194-036B-223	Sequence 223, App	C 201	13.2	73.3	1874	4	US-09-270-767-11069	Sequence 11069, A
C 129	13.2	73.3	361	4	US-09-270-767-447	Sequence 447, App	C 202	13.2	73.3	1874	4	US-08-469-242-3	Sequence 3, Appl
C 130	13.2	73.3	361	4	US-09-270-767-15729	Sequence 15729, A	C 203	13.2	73.3	1876	4	US-08-967-506-10	Sequence 10, Appl
C 131	13.2	73.3	362	4	US-09-270-767-29766	Sequence 29766, A	C 204	13.2	73.3	2125	3	US-09-109-004-5	Sequence 5, Appli
C 132	13.2	73.3	363	4	US-09-513-999C-22211	Sequence 22211, A	C 205	13.2	73.3	2150	4	US-09-862-660-1	Sequence 1, Appli
C 133	13.2	73.3	371	4	US-10-101-464A-464	Sequence 464, App	C 206	13.2	73.3	2253	4	US-09-107-532A-2214	Sequence 2214, Ap
C 134	13.2	73.3	392	4	US-09-513-999C-28478	Sequence 28478, A	C 207	13.2	73.3	2286	4	US-09-963-137-166	Sequence 166, App
C 135	13.2	73.3	483	4	US-09-107-532A-3610	Sequence 3610, Ap	C 208	13.2	73.3	2294	2	US-08-967-506-10	Sequence 10, Appl
C 136	13.2	73.3	496	4	US-09-621-976-17428	Sequence 17428, A	C 209	13.2	73.3	2294	3	PCT-US94-03552-10	Sequence 10, Appl
C 137	13.2	73.3	500	4	US-09-866-108A-15715	Sequence 15715, A	C 210	13.2	73.3	2294	5	US-09-963-137-212	Sequence 212, App
C 138	13.2	73.3	522	4	US-09-107-532A-3475	Sequence 3475, Ap	C 211	13.2	73.3	2304	4	US-09-583-110-1278	Sequence 1278, Ap
C 139	13.2	73.3	522	4	US-09-621-976-2440	Sequence 2440, Ap	C 212	13.2	73.3	2367	4	US-09-614-321A-419	Sequence 419, App
C 140	13.2	73.3	538	4	US-09-495-050A-105	Sequence 105, App	C 213	13.2	73.3	2460	1	US-07-795-859B-1	Sequence 1, Appli
C 141	13.2	73.3	569	3	US-09-109-204-15	Sequence 15, Appl	C 214	13.2	73.3	2470	1	US-08-457-616-1	Sequence 1, Appli
C 142	13.2	73.3	569	4	US-09-490-032-15	Sequence 15, Appl	C 215	13.2	73.3	2470	1	US-08-208-887A-48	Sequence 48, Appl
C 143	13.2	73.3	639	3	US-09-385-982-67	Sequence 67, Appl	C 216	13.2	73.3	2556	1	US-09-280-598-17	Sequence 17, Appl
C 144	13.2	73.3	639	4	US-09-134-000C-586	Sequence 586, App	C 217	13.2	73.3	2556	3	US-09-228-986-8	Sequence 8, Appli
C 145	13.2	73.3	777	4	US-09-270-767-31297	Sequence 31297, A	C 218	13.2	73.3	2638	3	US-10-101-464A-8	Sequence 8, Appli
C 146	13.2	73.3	820	4	US-09-540-236-1105	Sequence 1105, Ap	C 219	13.2	73.3	2778	4	US-09-924-097A-12	Sequence 12, Appl
C 147	13.2	73.3	824	4	US-09-270-767-15013	Sequence 15013, A	C 220	13.2	73.3	2795	4	US-09-688-188B-25	Sequence 25, Appl
C 148	13.2	73.3	828	4	US-09-252-991A-13980	Sequence 13980, A	C 221	13.2	73.3	2962	4	US-09-688-188B-106	Sequence 106, App
C 149	13.2	73.3	828	4	US-09-583-110-345	Sequence 345, App	C 222	13.2	73.3	3210	4	US-09-328-352-1348	Sequence 1348, Ap
C 150	13.2	73.3	885	4	US-09-400-236-471	Sequence 471, App	C 223	13.2	73.3	3216	4	US-09-814-915A-25	Sequence 25, Appl
C 151	13.2	73.3	885	4	US-10-101-464A-965	Sequence 965, App	C 224	13.2	73.3	3216	4	US-09-684-405-5	Sequence 5, Appli
C 152	13.2	73.3	899	4	US-09-284-526-3	Sequence 3, Appli	C 225	13.2	73.3	3216	4	US-08-464-402-1	Sequence 1, Appli
C 153	13.2	73.3	960	4	US-09-107-532A-1944	Sequence 1944, Ap	C 226	13.2	73.3	3417	2	US-09-054-775C-1	Sequence 1, Appli
C 154	13.2	73.3	1017	4	US-09-489-039A-5261	Sequence 5261, Ap	C 227	13.2	73.3	3417	4	US-09-221-017B-904	Sequence 904, App
C 155	13.2	73.3	1018	4	US-09-699-266A-1	Sequence 1, Appli	C 228	13.2	73.3	3571	4	US-09-328-352-1578	Sequence 1578, Ap
C 156	13.2	73.3	1056	4	US-09-919-039-160	Sequence 160, App	C 229	13.2	73.3	3702	4	US-08-762-308-11	Sequence 11, Appl
C 157	13.2	73.3	1114	4	US-09-876-594-412	Sequence 412, App	C 230	13.2	73.3	3796	2	US-09-844-634-10	Sequence 10, Appl
C 158	13.2	73.3	1116	4	US-09-614-912-173	Sequence 173, App	C 231	13.2	73.3	3796	4	US-08-650-000-3	Sequence 3, Appli
C 159	13.2	73.3	1218	3	US-09-154-874-7	Sequence 7, Appli	C 232	13.2	73.3	3813	4	US-09-758-124-3	Sequence 3, Appli
C 160	13.2	73.3	1218	4	US-08-931-668-7	Sequence 7, Appli	C 233	13.2	73.3	3813	6	5395760-3	Patent No. 5395760
C 161	13.2	73.3	1218	4	US-09-468-175-7	Sequence 7, Appli	C 234	13.2	73.3	3813	4	US-09-149-476-296	Sequence 296, App
C 162	13.2	73.3	1254	4	US-09-328-353-2855	Sequence 2855, Ap	C 235	13.2	73.3	3865	4	US-09-643-597-134	Sequence 134, App
C 163	13.2	73.3	1277	4	US-09-270-767-13742	Sequence 13742, A	C 236	13.2	73.3	4797	4	US-09-480-884A-134	Sequence 134, App
C 164	13.2	73.3	1297	3	US-09-446-821A-3	Sequence 3, Appli	C 237	13.2	73.3	4797	4	US-09-542-615A-134	Sequence 134, App
C 165	13.2	73.3	1305	6	5212087-1	Patent No. 5212087	C 238	13.2	73.3	4797	4	US-09-606-421B-134	Sequence 134, App
C 166	13.2	73.3	1308	3	US-09-724-864-15	Sequence 15, Appl	C 239	13.2	73.3	4797	4	US-09-221-107-134	Sequence 134, App
C 167	13.2	73.3	1332	4	US-09-328-352-3440	Sequence 3440, Ap	C 240	13.2	73.3	4797	4	US-09-466-396A-134	Sequence 134, App
C 168	13.2	73.3	1380	4	US-09-543-681A-3664	Sequence 3664, Ap	C 241	13.2	73.3	4797	4	US-08-476-496A-134	Sequence 134, App
C 169	13.2	73.3	1413	4	US-09-328-353-2786	Sequence 2786, Ap	C 242	13.2	73.3	4797	4	US-09-630-940B-134	Sequence 134, App
C 170	13.2	73.3	1470	3	US-09-134-001C-83	Sequence 83, Appl	C 243	13.2	73.3	4797	4	US-08-210-535-5	Sequence 5, Appli
C 171	13.2	73.3	1480	1	US-08-448-736-11	Sequence 11, Appl	C 244	13.2	73.3	4797	4		
C 172	13.2	73.3	1480	1	US-08-452-736-11	Sequence 11, Appl	C 245	13.2	73.3	4797	4		
C 173	13.2	73.3	1480	1	US-08-445-065-11	Sequence 11, Appl	C 246	13.2	73.3	4797	2		

247	13.2	73.3	4899	6	526270-1	Patent No. 526270	12.8	71.1	389	4	US-09-621-976-3333	Sequence 3333, Ap
248	13.2	73.3	5275	1	US-08-485-588-1	Sequence 1, Appl	12.8	71.1	409	3	US-09-328-111-669	Sequence 669, App
249	13.2	73.3	5275	1	US-08-484-565-1	Sequence 1, Appl	12.8	71.1	409	3	US-08-986-471E-1163	Sequence 1163, Ap
250	13.2	73.3	5275	1	US-08-480-751-1	Sequence 1, Appl	12.8	71.1	409	4	US-08-781-986A-1163	Sequence 1163, Ap
251	13.2	73.3	5275	2	US-08-943-986-1	Sequence 1, Appl	12.8	71.1	416	4	US-09-513-999C-11292	Sequence 11292, A
252	13.2	73.3	5275	3	US-08-353-784-1	Sequence 1, Appl	12.8	71.1	540	4	US-09-134-000C-798	Sequence 798, App
253	13.2	73.3	5275	3	US-08-484-7198-1	Sequence 1, Appl	12.8	71.1	565	4	US-09-589-733C-6	Sequence 614, Appl
254	13.2	73.3	5275	3	US-08-484-159-1	Sequence 1, Appl	12.8	71.1	578	4	US-09-023-655-614	Sequence 614, Appl
255	13.2	73.3	5416	4	US-09-284-926-8	Sequence 8, Appl	12.8	71.1	626	4	US-09-527-223-1	Sequence 1, Appl
256	13.2	73.3	5430	3	US-09-012-515A-11	Sequence 11, Appl	12.8	71.1	649	3	US-09-328-111-314	Sequence 314, Appl
257	13.2	73.3	5430	3	US-08-360-144A-11	Sequence 11, Appl	12.8	71.1	687	4	US-09-540-236-1382	Sequence 1382, Ap
258	13.2	73.3	5430	4	US-09-012-504A-11	Sequence 11, Appl	12.8	71.1	693	4	US-09-248-796A-1697	Sequence 1697, Ap
259	13.2	73.3	5430	4	US-09-012-399A-11	Sequence 11, Appl	12.8	71.1	708	4	US-09-107-532A-121	Sequence 121, App
260	13.2	73.3	5658	3	US-08-881-450A-23	Sequence 23, Appl	12.8	71.1	729	4	US-09-583-110-307	Sequence 307, App
261	13.2	73.3	5737	1	US-08-439-264-1	Sequence 1, Appl	12.8	71.1	780	4	US-08-990-823-70	Sequence 70, Appl
262	13.2	73.3	5813	4	US-09-495-714C-1	Sequence 1, Appl	12.8	71.1	816	3	US-09-477-135A-70	Sequence 68, Appl
263	13.2	73.3	6029	3	US-09-149-727-1	Sequence 1, Appl	12.8	71.1	816	3	US-09-399-913-68	Sequence 68, Appl
264	13.2	73.3	6088	4	US-09-799-451-730	Sequence 730, App	12.8	71.1	816	3	US-09-350-614-68	Sequence 246, Ap
265	13.2	73.3	6112	4	US-09-495-714C-3	Sequence 3, Appl	12.8	71.1	843	4	US-09-583-110-2546	Sequence 152, App
266	13.2	73.3	7653	4	US-08-471-112A-1	Sequence 1, Appl	12.8	71.1	905	4	US-08-961-527-152	Sequence 26942, A
267	13.2	73.3	7653	4	US-09-950-634-1	Sequence 1, Appl	12.8	71.1	1005	4	US-09-270-767-26942	Sequence 155, App
268	13.2	73.3	7824	5	US-09-950-634-1	Sequence 1, Appl	12.8	71.1	1068	4	US-09-248-796A-155	Sequence 155, App
269	13.2	73.3	13188	4	US-08-961-527-70	Sequence 70, Appl	12.8	71.1	1128	4	US-09-328-352-1952	Sequence 1952, Ap
270	13.2	73.3	16995	4	US-08-961-527-82	Sequence 82, Appl	12.8	71.1	1208	4	US-09-270-767-26942	Sequence 26942, A
271	13.2	73.3	31063	4	US-09-596-002-20	Sequence 20, Appl	12.8	71.1	1299	4	US-09-270-767-26942	Sequence 152, App
272	13.2	73.3	35881	4	US-08-311-731A-127	Sequence 127, App	12.8	71.1	1386	4	US-09-270-767-26942	Sequence 155, App
273	13.2	73.3	35881	4	US-08-453-702B-50	Sequence 50, Appl	12.8	71.1	1533	4	US-09-484-970B-123	Sequence 123, App
274	13.2	73.3	42325	4	US-08-311-731A-131	Sequence 131, App	12.8	71.1	1620	3	US-09-614-221A-201	Sequence 201, App
275	13.2	73.3	59065	3	US-09-813-817-3	Sequence 3, Appl	12.8	71.1	1655	1	US-09-360-197-3	Sequence 3, Appl
276	13.2	73.3	59065	3	US-09-813-817-3	Sequence 3, Appl	12.8	71.1	1655	1	US-07-984-044A-2	Sequence 2, Appl
277	13.2	73.3	59065	4	US-09-978-197-3	Sequence 3, Appl	12.8	71.1	1701	4	US-08-458-393-2	Sequence 2, Appl
278	13.2	73.3	59065	4	US-09-978-197-3	Sequence 3, Appl	12.8	71.1	1782	1	US-08-742-273-1	Sequence 1, Appl
279	13.2	73.3	59065	4	US-10-135-696-3	Sequence 3, Appl	12.8	71.1	1837	4	US-09-270-767-7629	Sequence 7629, Ap
280	13.2	73.3	59065	4	US-10-135-696-3	Sequence 3, Appl	12.8	71.1	1837	4	US-09-270-767-7629	Sequence 22911, A
281	13.2	73.3	62909	4	US-09-596-002-32	Sequence 32, Appl	12.8	71.1	1842	4	US-09-614-221A-538	Sequence 538, App
282	13.2	73.3	70559	4	US-09-409-800B-1	Sequence 1, Appl	12.8	71.1	1908	4	US-09-614-221A-223	Sequence 223, App
283	13.2	73.3	80246	3	US-09-078-294-4	Sequence 4, Appl	12.8	71.1	1921	4	US-09-057-986-7	Sequence 7, Appl
284	13.2	73.3	80595	3	US-09-754-250-3	Sequence 3, Appl	12.8	71.1	1958	4	US-09-270-767-10139	Sequence 10139, A
285	13.2	73.3	111282	3	US-09-754-250-3	Sequence 3, Appl	12.8	71.1	2016	3	US-09-132-118-1	Sequence 1, Appl
286	13.2	73.3	246240	2	US-08-724-394A-20	Sequence 20, Appl	12.8	71.1	2016	3	US-09-302-769-24	Sequence 24, Appl
287	13.2	73.3	246240	2	US-08-724-394A-22	Sequence 22, Appl	12.8	71.1	2104	1	US-08-592-126-96	Sequence 96, Appl
288	13.2	73.3	320000	4	US-10-027-983-11	Sequence 11, Appl	12.8	71.1	2104	1	US-09-168-595-96	Sequence 16, Appl
289	13.2	73.3	380073	3	US-09-545-528D-1	Sequence 1, Appl	12.8	71.1	2137	1	US-08-444-005-16	Sequence 331, App
290	13.2	73.3	4403765	3	US-09-103-840A-2	Sequence 2, Appl	12.8	71.1	2168	4	US-09-907-794A-331	Sequence 331, App
291	13.2	73.3	4403765	3	US-09-103-840A-2	Sequence 2, Appl	12.8	71.1	2168	4	US-09-908-125A-331	Sequence 331, App
292	13.2	73.3	4403765	3	US-09-103-840A-2	Sequence 2, Appl	12.8	71.1	2168	4	US-09-902-775A-331	Sequence 331, App
293	13.2	73.3	4411529	3	US-09-103-840A-1	Sequence 1, Appl	12.8	71.1	2168	4	US-09-906-700-331	Sequence 331, App
294	13.2	73.3	4411529	3	US-09-103-840A-1	Sequence 1, Appl	12.8	71.1	2168	4	US-09-903-603A-331	Sequence 331, App
295	13.2	73.3	4411529	3	US-09-103-840A-1	Sequence 1, Appl	12.8	71.1	2194	2	US-08-633-879C-3	Sequence 3, Appl
296	13.2	73.3	4411529	3	US-08-501-126-13	Sequence 13, Appl	12.8	71.1	2227	3	US-09-071-709-5	Sequence 5, Appl
297	13.2	73.3	327	4	US-09-248-796A-6935	Sequence 6935, Ap	12.8	71.1	2369	4	US-09-057-996-13	Sequence 13, Appl
298	13.2	73.3	394	4	US-09-513-999C-27193	Sequence 27193, A	12.8	71.1	2372	4	US-09-057-996-15	Sequence 15, Appl
299	13.2	73.3	435	4	US-09-248-796A-11060	Sequence 11060, A	12.8	71.1	2436	4	US-09-540-236-492	Sequence 492, App
300	13.2	73.3	896	4	US-09-404-879A-22	Sequence 22, Appl	12.8	71.1	2440	3	US-08-724-984A-1	Sequence 1, Appl
301	13.2	73.3	896	4	US-09-338-833-22	Sequence 22, Appl	12.8	71.1	2460	4	US-09-270-767-11376	Sequence 11376, A
302	13.2	73.3	896	4	US-09-215-681-22	Sequence 22, Appl	12.8	71.1	2480	4	US-09-789-273-1	Sequence 1, Appl
303	13.2	73.3	896	4	US-09-215-681-22	Sequence 22, Appl	12.8	71.1	2533	4	US-09-482-273-59	Sequence 59, Appl
304	13.2	73.3	3207	4	US-08-667-857-22	Sequence 22, Appl	12.8	71.1	2596	3	US-09-289-254-1	Sequence 1, Appl
305	12.8	71.1	161	4	US-09-248-796A-4563	Sequence 4563, Ap	12.8	71.1	2597	3	US-09-620-312D-48	Sequence 48, Appl
306	12.8	71.1	203	4	US-09-270-767-29514	Sequence 29514, A	12.8	71.1	2617	3	US-09-161-443-1	Sequence 1, Appl
307	12.8	71.1	203	4	US-09-513-999C-24868	Sequence 24868, A	12.8	71.1	2617	3	US-09-023-655-914	Sequence 914, App
308	12.8	71.1	203	4	US-09-513-999C-25235	Sequence 25235, A	12.8	71.1	2617	4	US-09-056-285A-4	Sequence 4, Appl
309	12.8	71.1	245	4	US-09-513-999C-10344	Sequence 10344, A	12.8	71.1	2800	3	US-09-651-656-4	Sequence 4, Appl
310	12.8	71.1	247	4	US-09-416-434-549	Sequence 36644, A	12.8	71.1	2805	3	US-09-650-855-4	Sequence 1, Appl
311	12.8	71.1	279	4	US-09-360-376-32	Sequence 32, Appl	12.8	71.1	2805	3	US-08-457-176-1	Sequence 1, Appl
312	12.8	71.1	282	4	US-09-360-376-304	Sequence 304, Ap	12.8	71.1	2947	1	US-08-457-176-1	Sequence 1, Appl
313	12.8	71.1	288	4	US-09-360-376-304	Sequence 304, Ap	12.8	71.1	2947	1	US-08-457-176-1	Sequence 1, Appl
314	12.8	71.1	288	4	US-09-360-376-304	Sequence 304, Ap	12.8	71.1	2947	1	US-08-457-176-1	Sequence 1, Appl
315	12.8	71.1	309	2	US-09-513-999C-1956	Sequence 1956, Ap	12.8	71.1	3096	5	US-09-620-312D-48	Sequence 48, Appl
316	12.8	71.1	313	4	US-08-633-879C-13	Sequence 13, Appl	12.8	71.1	3145	4	US-09-023-655-914	Sequence 914, App
317	12.8	71.1	357	4	US-09-401-064-271	Sequence 271, App	12.8	71.1	3145	4	US-09-056-285A-4	Sequence 4, Appl
318	12.8	71.1	380	4	US-09-621-976-13121	Sequence 13121, A	12.8	71.1	3145	4	US-09-788-200-14	Sequence 14, Appl
319	12.8	71.1	383	4	US-09-513-999C-11291	Sequence 11291, A	12.8	71.1	3145	4	US-09-788-200-14	Sequence 14, Appl
320	12.8	71.1	383	4	US-09-270-767-13523	Sequence 13523, A	12.8	71.1	3243	1	US-09-712-691-12	Sequence 12, Appl
321	12.8	71.1	383	4	US-09-270-767-13523	Sequence 13523, A	12.8	71.1	3243	1	US-08-611-107-32	Sequence 32, Appl



C 393	12.8	71.1	3318	4	US-09-540-236-1379	Sequence 1379, App	466	12.4	68.9	420	4	US-09-513-995C-3452	Sequence 3452, Ap
C 394	12.8	71.1	3376	4	US-09-620-312D-918	Sequence 918, App	467	12.4	68.9	435	4	US-09-270-767-4624	Sequence 4624, Ap
C 395	12.8	71.1	3937	4	US-09-620-312D-280	Sequence 280, App	468	12.4	68.9	435	4	US-09-270-767-19906	Sequence 19906, A
C 396	12.8	71.1	4079	4	US-09-616-434-1247	Sequence 1247, App	469	12.4	68.9	463	1	US-07-695-564-10	Sequence 10, Appl
C 397	12.8	71.1	4414	5	PCT-US95-04567-1	Sequence 1, Appli	C 470	12.4	68.9	463	1	US-08-241-387-10	Sequence 10, Appl
C 398	12.8	71.1	4808	4	US-09-774-528-19	Sequence 19, Appl	471	12.4	68.9	470	2	US-08-967-101-99	Sequence 99, Appl
C 399	12.8	71.1	5323	4	US-09-799-451-726	Sequence 726, App	472	12.4	68.9	470	2	US-08-592-541-99	Sequence 99, Appl
C 400	12.8	71.1	5438	3	US-08-456-200B-5	Sequence 5, Appli	473	12.4	68.9	470	3	US-09-124-688-99	Sequence 99, Appl
C 401	12.8	71.1	5761	4	US-09-798-451-23	Sequence 23, Appl	474	12.4	68.9	470	3	US-09-124-688-99	Sequence 99, Appl
C 402	12.8	71.1	5709	3	US-08-285-601-3	Sequence 3, Appli	475	12.4	68.9	470	3	US-09-124-688-99	Sequence 99, Appl
C 403	12.8	71.1	7010	4	US-09-555-510B-11	Sequence 11, Appl	476	12.4	68.9	470	3	US-08-496-841C-99	Sequence 99, Appl
C 404	12.8	71.1	7010	4	US-10-231-013-11	Sequence 11, Appl	477	12.4	68.9	470	3	US-09-124-523-99	Sequence 99, Appl
C 405	12.8	71.1	7263	4	US-09-562-702A-31	Sequence 31, Appl	478	12.4	68.9	470	4	US-09-636-796A-99	Sequence 99, Appl
C 406	12.8	71.1	7263	4	US-09-561-818A-27	Sequence 27, Appl	479	12.4	68.9	470	4	US-08-431-048F-99	Sequence 99, Appl
C 407	12.8	71.1	7554	4	US-09-562-702A-29	Sequence 29, Appl	480	12.4	68.9	472	4	US-09-702-705-11	Sequence 11, Appl
C 408	12.8	71.1	7554	4	US-09-561-818A-25	Sequence 25, Appl	481	12.4	68.9	472	4	US-09-736-457-11	Sequence 11, Appl
C 409	12.8	71.1	8220	4	US-08-797-908-3	Sequence 3, Appli	482	12.4	68.9	472	4	US-09-614-124B-11	Sequence 11, Appl
C 410	12.8	71.1	9687	3	US-09-133-944-2	Sequence 2, Appli	483	12.4	68.9	472	4	US-09-671-325-11	Sequence 11, Appl
C 411	12.8	71.1	9687	3	US-09-208-827-2	Sequence 2, Appli	484	12.4	68.9	472	4	US-09-589-184-11	Sequence 11, Appl
C 412	12.8	71.1	9687	4	US-10-043-074-2	Sequence 2, Appli	C 485	12.4	68.9	489	4	US-09-658-824-11	Sequence 11, Appl
C 413	12.8	71.1	9707	4	US-08-961-527-164	Sequence 164, App	C 486	12.4	68.9	491	4	US-09-248-796A-14088	Sequence 14088, A
C 414	12.8	71.1	11309	4	US-08-961-527-108	Sequence 108, App	C 487	12.4	68.9	517	3	US-09-513-996C-31611	Sequence 31611, A
C 415	12.8	71.1	14796	3	US-08-975-080-35	Sequence 35, Appl	C 488	12.4	68.9	535	1	US-09-276-531-122	Sequence 122, App
C 416	12.8	71.1	14796	3	US-08-630-706-10	Sequence 10, Appl	C 489	12.4	68.9	535	1	US-08-742-023-1	Sequence 1, Appli
C 417	12.8	71.1	14796	3	US-09-496-694B-3	Sequence 3, Appli	C 490	12.4	68.9	568	3	US-08-968-505-1	Sequence 9, Appli
C 418	12.8	71.1	20137	3	US-09-262-773-206	Sequence 206, App	C 491	12.4	68.9	568	4	US-09-546-049-9	Sequence 9, Appli
C 419	12.8	71.1	20138	3	US-09-262-773-9	Sequence 9, Appli	C 492	12.4	68.9	657	3	US-09-039-982A-38	Sequence 38, Appl
C 420	12.8	71.1	20966	4	US-09-984-880-3	Sequence 3, Appli	C 493	12.4	68.9	657	3	US-09-039-641-38	Sequence 38, Appl
C 421	12.8	71.1	20966	4	US-10-277-032-3	Sequence 3, Appli	C 494	12.4	68.9	657	3	US-09-039-762A-38	Sequence 38, Appl
C 422	12.8	71.1	23071	3	US-08-262-773-210	Sequence 210, App	C 495	12.4	68.9	657	3	US-08-042-452D-38	Sequence 38, Appl
C 423	12.8	71.1	28958	1	US-08-258-261B-6	Sequence 6, Appli	C 496	12.4	68.9	667	3	US-08-998-416-1147	Sequence 1147, Ap
C 424	12.8	71.1	28958	1	US-08-456-837-6	Sequence 6, Appli	C 497	12.4	68.9	723	3	US-08-466-465-3	Sequence 3, Appli
C 425	12.8	71.1	28958	1	US-08-457-342-6	Sequence 6, Appli	C 498	12.4	68.9	723	3	US-08-466-465-3	Sequence 3, Appli
C 426	12.8	71.1	28958	1	US-08-457-646A-6	Sequence 6, Appli	C 499	12.4	68.9	726	3	US-09-730-465-3	Sequence 37, Appl
C 427	12.8	71.1	28958	1	US-08-458-076A-6	Sequence 6, Appli	C 500	12.4	68.9	726	3	US-09-039-982A-37	Sequence 37, Appl
C 428	12.8	71.1	28958	1	US-08-764-233A-4	Sequence 4, Appli	C 501	12.4	68.9	726	3	US-09-039-641-37	Sequence 37, Appl
C 429	12.8	71.1	28958	1	US-08-457-335A-6	Sequence 6, Appli	C 502	12.4	68.9	726	3	US-09-039-762A-37	Sequence 37, Appl
C 430	12.8	71.1	28958	1	US-08-729-214-6	Sequence 6, Appli	C 503	12.4	68.9	726	3	US-09-042-452D-37	Sequence 37, Appl
C 431	12.8	71.1	28958	3	US-09-028-934-6	Sequence 6, Appli	C 504	12.4	68.9	726	4	US-08-913-612A-37	Sequence 37, Appl
C 432	12.8	71.1	38584	3	US-09-453-702B-50	Sequence 50, Appl	C 505	12.4	68.9	751	4	US-09-621-976-3052	Sequence 3052, Ap
C 433	12.8	71.1	45613	4	US-09-596-002-27	Sequence 27, Appl	C 506	12.4	68.9	753	1	US-08-328-152A-16	Sequence 16, Appl
C 434	12.8	71.1	48908	3	US-09-453-702B-137	Sequence 137, App	C 507	12.4	68.9	753	4	US-08-466-465-1	Sequence 1, Appli
C 435	12.8	71.1	49377	1	US-08-764-233A-1	Sequence 1, Appli	C 508	12.4	68.9	753	4	US-09-730-465-1	Sequence 1, Appli
C 436	12.8	71.1	61663	4	US-09-453-702B-62	Sequence 62, Appl	C 509	12.4	68.9	821	3	US-08-858-207A-195	Sequence 19578, A
C 437	12.8	71.1	65792	4	US-09-536-002-31	Sequence 31, Appl	C 510	12.4	68.9	852	1	US-09-621-976-15578	Sequence 21, Appl
C 438	12.8	71.1	66933	4	US-09-544-398B-11	Sequence 11, Appl	C 511	12.4	68.9	852	2	US-08-075-533-21	Sequence 21, Appl
C 439	12.8	71.1	66933	4	US-09-543-771-11	Sequence 11, Appl	C 512	12.4	68.9	852	2	US-08-948-176-21	Sequence 21, Appl
C 440	12.8	71.1	72049	4	US-09-544-398B-9	Sequence 9, Appli	C 513	12.4	68.9	852	5	PCT-US91-09160-21	Sequence 21, Appl
C 441	12.8	71.1	72049	4	US-09-543-771-9	Sequence 9, Appli	C 514	12.4	68.9	855	6	5185441-40	Patent No. 5185441
C 442	12.8	71.1	72604	3	US-09-568-992-7	Sequence 7, Appli	C 515	12.4	68.9	855	6	5223394-3	Patent No. 5223394
C 443	12.8	71.1	72604	3	US-09-567-474-7	Sequence 7, Appli	C 516	12.4	68.9	857	4	US-09-270-767-28776	Sequence 28776, A
C 444	12.8	71.1	74962	4	US-09-685-853A-3	Sequence 3, Appli	C 517	12.4	68.9	863	1	US-07-940-861-11	Sequence 11, Appl
C 445	12.8	71.1	99629	4	US-09-596-002-37	Sequence 37, Appl	C 518	12.4	68.9	863	2	US-08-459-512-11	Sequence 11, Appl
C 446	12.8	71.1	99629	4	US-09-596-002-37	Sequence 37, Appl	C 519	12.4	68.9	863	2	US-08-459-512-11	Sequence 11, Appl
C 447	12.8	71.1	536165	4	US-09-214-808-1	Sequence 1, Appli	C 520	12.4	68.9	863	5	US-08-460-132-11	Sequence 11, Appl
C 448	12.8	71.1	1830121	4	US-09-557-884-1	Sequence 1, Appli	C 521	12.4	68.9	863	5	PCT-US92-02050-11	Sequence 11, Appl
C 449	12.8	71.1	1830121	4	US-09-643-990A-1	Sequence 1, Appli	C 522	12.4	68.9	863	6	5185441-35	Patent No. 5185441
C 450	12.8	71.1	1830121	4	US-10-329-960-1	Sequence 1, Appli	C 523	12.4	68.9	863	6	5223394-5	Patent No. 5223394
C 451	12.4	68.9	25	4	US-09-368-743-8	Sequence 8, Appli	C 524	12.4	68.9	865	1	US-08-075-533-22	Sequence 22, Appl
C 452	12.4	68.9	25	4	US-10-044-543-8	Sequence 8, Appli	C 525	12.4	68.9	865	2	US-08-948-176-22	Sequence 22, Appl
C 453	12.4	68.9	239	4	US-09-016-434-844	Sequence 844, App	C 526	12.4	68.9	865	5	PCT-US91-09160-22	Sequence 22, Appl
C 454	12.4	68.9	263	4	US-09-513-999C-10130	Sequence 10130, A	C 527	12.4	68.9	874	4	US-08-756-416-37	Sequence 37, Appl
C 455	12.4	68.9	286	4	US-09-313-294A-2180	Sequence 2180, Ap	C 528	12.4	68.9	879	4	US-09-270-767-25642	Sequence 25642, A
C 456	12.4	68.9	315	1	US-08-328-152A-29	Sequence 29, Appl	C 529	12.4	68.9	894	4	US-09-328-352-3915	Sequence 3915, Ap
C 457	12.4	68.9	315	1	US-08-328-152A-23	Sequence 23, Appl	C 530	12.4	68.9	898	4	US-09-976-594-1003	Sequence 1003, Ap
C 458	12.4	68.9	336	1	US-08-328-152A-23	Sequence 23, Appl	C 531	12.4	68.9	906	4	US-09-583-110-2451	Sequence 110, Appl
C 459	12.4	68.9	336	4	US-08-956-171B-4434	Sequence 4434, Ap	C 532	12.4	68.9	956	4	US-09-610-185C-1	Sequence 1, Appli
C 460	12.4	68.9	336	4	US-08-781-986A-4434	Sequence 4434, Ap	C 533	12.4	68.9	969	4	US-09-023-655-66	Sequence 66, Appl
C 461	12.4	68.9	361	4	US-09-513-999C-3637	Sequence 3637, Ap	C 534	12.4	68.9	987	4	US-09-540-236-619	Sequence 619, App
C 462	12.4	68.9	402	1	US-09-513-999C-13365	Sequence 13365, A	C 535	12.4	68.9	1011	4	US-09-107-532A-584	Sequence 584, App
C 463	12.4	68.9	402	1	US-08-328-152A-12	Sequence 12, Appl	C 536	12.4	68.9	1033	4	US-09-610-185C-3	Sequence 3, Appli
C 464	12.4	68.9	402	1	US-09-513-999C-16705	Sequence 16705, A	C 537	12.4	68.9	1040	1	US-07-940-861-9	Sequence 9, Appli
C 465	12.4	68.9	408	1	US-08-328-152A-22	Sequence 22, Appl	C 538	12.4	68.9	1040	1	US-08-459-512-9	Sequence 9, Appli

C 539	12.4	68.9	1040	2	US-08-459-657-9	Sequence 9, Appli	C 612	12.4	68.9	2385	3	US-08-185-359-9	Sequence 9, Appli
C 540	12.4	68.9	1040	3	US-08-460-132-9	Sequence 1, Appli	C 613	12.4	68.9	2434	3	US-09-272-496-1	Sequence 1, Appli
C 541	12.4	68.9	1040	3	US-09-045-106-1	Sequence 1, Appli	C 614	12.4	68.9	2448	2	US-09-620-3120-64	Sequence 64, Appl
C 542	12.4	68.9	1040	4	US-09-023-655-1341	Sequence 1341, Ap	C 615	12.4	68.9	2450	2	US-08-463-0818-5	Sequence 5, Appli
C 543	12.4	68.9	1040	5	PCT-US92-02050-9	Sequence 9, Appli	C 616	12.4	68.9	2450	2	US-08-461-3798-5	Sequence 5, Appli
C 544	12.4	68.9	1040	6	P185441-39	Patent No. 5185441	C 617	12.4	68.9	2450	3	US-08-462-3908-5	Sequence 5, Appli
C 545	12.4	68.9	1040	6	5223394-2	Patent No. 5223394	C 618	12.4	68.9	2450	3	US-08-463-0748-5	Sequence 5, Appli
C 546	12.4	68.9	1044	4	US-09-248-796A-6259	Sequence 6259, Ap	C 619	12.4	68.9	2450	3	US-08-465-5850-5	Sequence 5, Appli
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C 552	12.4	68.9	1050	3	US-09-730-465-7	Sequence 7, Appli	C 625	12.4	68.9	2797	2	US-09-123-465-4	Sequence 4, Appli
C 553	12.4	68.9	1050	5	PCT-US92-02050-42	Sequence 42, Appl	C 626	12.4	68.9	2797	2	US-09-123-465-4	Sequence 4, Appli
C 554	12.4	68.9	1062	4	US-09-802-117-3	Sequence 3, Appli	C 627	12.4	68.9	2862	4	US-09-270-767-12914	Sequence 12914, A
C 555	12.4	68.9	1095	3	US-08-928-3838-3	Sequence 3, Appli	C 628	12.4	68.9	2874	4	US-09-620-3120-10	Sequence 10, Appl
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C 557	12.4	68.9	1191	2	US-08-968-751-5	Sequence 5, Appli	C 630	12.4	68.9	3069	4	US-09-620-3120-11	Sequence 11, Appl
C 558	12.4	68.9	1273	3	US-08-722-184-5	Sequence 5, Appli	C 631	12.4	68.9	3279	4	US-09-620-3120-11	Sequence 11, Appl
C 559	12.4	68.9	1302	4	US-09-043-937A-9	Sequence 329, App	C 632	12.4	68.9	3892	2	US-09-555-7238-3	Sequence 3, Appli
C 560	12.4	68.9	1317	4	US-09-614-221A-329	Sequence 3152, Ap	C 633	12.4	68.9	3892	2	US-09-123-465-3	Sequence 3, Appli
C 561	12.4	68.9	1374	1	US-08-123-761A-2	Sequence 2, Appli	C 634	12.4	68.9	3892	4	US-09-799-451-250	Sequence 250, App
C 562	12.4	68.9	1374	1	US-08-123-761A-2	Sequence 2, Appli	C 635	12.4	68.9	3981	4	US-09-016-434-1222	Sequence 4, Appli
C 563	12.4	68.9	1383	4	US-09-107-532A-2617	Sequence 2617, Ap	C 636	12.4	68.9	4079	4	US-08-945-056-4	Sequence 4, Appli
C 564	12.4	68.9	1464	4	US-09-328-352-2641	Sequence 2641, Ap	C 637	12.4	68.9	4201	3	US-08-849-800A-3	Sequence 3, Appli
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C 567	12.4	68.9	1489	4	US-09-770-767-10275	Sequence 10275, A	C 640	12.4	68.9	4745	4	US-08-961-527-218	Sequence 218, App
C 568	12.4	68.9	1497	4	US-09-328-352-880	Sequence 880, App	C 641	12.4	68.9	5215	4	US-09-173-053-8	Sequence 8, Appli
C 569	12.4	68.9	1509	4	US-09-440-236-1860	Sequence 1860, Ap	C 642	12.4	68.9	5385	4	US-09-920-804-1	Sequence 1, Appli
C 570	12.4	68.9	1584	3	US-08-928-383B-1	Sequence 1, Appli	C 643	12.4	68.9	5889	4	US-09-402-923-3	Sequence 3, Appli
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C 572	12.4	68.9	1588	4	US-09-557-800-53	Sequence 53, Appl	C 645	12.4	68.9	6794	4	US-08-431-356C-2	Sequence 2, Appli
C 573	12.4	68.9	1623	3	US-09-433-994-1	Sequence 1, Appli	C 646	12.4	68.9	8876	4	US-08-961-527-170	Sequence 170, App
C 574	12.4	68.9	1623	3	US-09-583-110-698	Sequence 698, App	C 647	12.4	68.9	9062	4	US-08-956-171E-85	Sequence 85, Appl
C 575	12.4	68.9	1642	4	US-09-270-767-15160	Sequence 15160, A	C 648	12.4	68.9	9062	4	US-08-781-986A-85	Sequence 85, Appl
C 576	12.4	68.9	1662	3	US-09-738-894A-1	Sequence 1, Appli	C 649	12.4	68.9	9706	4	US-08-843-250-3	Sequence 3, Appli
C 577	12.4	68.9	1662	4	US-09-802-117-1	Sequence 1, Appli	C 650	12.4	68.9	9841	4	US-09-843-250-3	Sequence 3, Appli
C 578	12.4	68.9	1662	4	US-09-964-469-1	Sequence 1747, Ap	C 651	12.4	68.9	1462	4	US-08-961-527-26	Sequence 26, Appl
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C 581	12.4	68.9	1689	1	US-08-453-866-11	Sequence 8, Appli	C 654	12.4	68.9	33778	4	US-08-311-731A-132	Sequence 132, App
C 582	12.4	68.9	1753	3	US-08-750-134A-8	Sequence 8, Appli	C 655	12.4	68.9	36412	4	US-09-738-894A-3	Sequence 3, Appli
C 583	12.4	68.9	1753	3	US-09-363-745-8	Sequence 8, Appli	C 656	12.4	68.9	36551	3	US-09-964-469-3	Sequence 3, Appli
C 584	12.4	68.9	1763	4	US-09-620-3120-382	Sequence 382, App	C 657	12.4	68.9	50000	3	US-09-146-053-3	Sequence 2, Appli
C 585	12.4	68.9	1791	4	US-09-270-767-15179	Sequence 15179, A	C 658	12.4	68.9	51719	4	US-09-918-686-2	Sequence 2, Appli
C 586	12.4	68.9	1908	4	US-09-248-796A-1428	Sequence 1428, Ap	C 659	12.4	68.9	52998	4	US-09-491-356C-1	Sequence 1, Appli
C 587	12.4	68.9	2031	4	US-09-614-912-137	Sequence 137, App	C 660	12.4	68.9	81001	4	US-09-750-580-1	Sequence 1, Appli
C 588	12.4	68.9	2176	4	US-09-843-250-8	Sequence 8, Appli	C 661	12.4	68.9	107820	4	US-09-792-616-1	Sequence 1, Appli
C 589	12.4	68.9	2223	1	US-09-178-002-3	Sequence 3, Appli	C 662	12.4	68.9	92139	4	US-09-918-686-1	Sequence 1, Appli
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C 592	12.4	68.9	2265	4	US-09-843-250-1	Sequence 1, Appli	C 665	12.4	68.9	786431	4	US-09-198-452A-1	Sequence 1, Appli
C 593	12.4	68.9	2265	4	US-09-843-250-25	Sequence 25, Appl	C 666	12.4	68.9	1230025	4	US-09-557-884-1	Sequence 1, Appli
C 594	12.4	68.9	2265	4	US-09-843-250-27	Sequence 27, Appl	C 667	12.4	68.9	1830121	4	US-09-643-990A-1	Sequence 1, Appli
C 595	12.4	68.9	2265	4	US-09-843-250-28	Sequence 28, Appl	C 668	12.4	68.9	1830121	4	US-10-329-960-1	Sequence 5, Appli
C 596	12.4	68.9	2265	4	US-09-843-250-29	Sequence 29, Appl	C 669	12.4	68.9	21	4	US-09-403-690-5	Sequence 5, Appli
C 597	12.4	68.9	2265	4	US-09-843-250-30	Sequence 30, Appl	C 670	12.4	68.9	27	3	US-08-913-014A-19	Sequence 19, Appl
C 598	12.4	68.9	2265	4	US-09-843-250-31	Sequence 31, Appl	C 671	12.4	68.9	27	4	US-09-653-285-19	Sequence 19, Appl
C 599	12.4	68.9	2265	4	US-09-843-250-56	Sequence 56, Appl	C 672	12.4	68.9	54	4	US-08-956-171E-2329	Sequence 2329, Ap
C 600	12.4	68.9	2265	4	US-09-843-250-57	Sequence 57, Appl	C 673	12.4	68.9	54	4	US-08-781-986A-2329	Sequence 2329, Ap
C 601	12.4	68.9	2294	4	US-08-843-250-6	Sequence 6, Appli	C 674	12.4	68.9	61	3	US-08-863-813A-23	Sequence 23, Appl
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C 603	12.4	68.9	2296	3	US-09-267-423-3	Sequence 3, Appli	C 676	12.4	68.9	63	1	US-09-500-700-23	Sequence 23, Appl
C 604	12.4	68.9	2314	1	US-09-178-002-1	Sequence 1, Appli	C 677	12.4	68.9	63	1	US-07-627-323B-9	Sequence 9, Appli
C 605	12.4	68.9	2348	4	US-09-388-743-5	Sequence 5, Appli	C 678	12.4	68.9	63	1	US-07-988-754-9	Sequence 9, Appli
C 606	12.4	68.9	2348	4	US-10-044-543-5	Sequence 5, Appli	C 679	12.4	68.9	63	1	US-07-627-323-8	Sequence 8, Appli
C 607	12.4	68.9	2367	4	US-09-248-796A-650	Sequence 650, App	C 680	12.4	68.9	64	3	US-08-516-859A-95	Sequence 95, Appl
C 608	12.4	68.9	2372	4	US-09-016-434-1441	Sequence 1441, Ap	C 681	12.4	68.9	64	3	US-09-586-472-95	Sequence 95, Appl
C 609	12.4	68.9	2385	1	US-08-454-097-9	Sequence 9, Appli	C 682	12.4	68.9	66	3	US-09-528-706-95	Sequence 95, Appl
C 610	12.4	68.9	2385	1	US-08-468-036-41	Sequence 41, Appl	C 683	12.4	68.9	66	3	US-09-932-082-17	Sequence 17, Appl
C 611	12.4	68.9	2385	2	US-08-376-683-41	Sequence 41, Appl	C 684	12.4	68.9	66	4	US-09-861-687-17	Sequence 17, Appl

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686	12.2	67.8	68	4	US-09-861-687-16	Sequence 16, Appl	759	12.2	67.8	319	4	US-09-313-294A-7367	Sequence 7367, Ap
687	12.2	67.8	71	3	US-08-932-082-15	Sequence 15, Appl	760	12.2	67.8	328	4	US-09-513-999C-19797	Sequence 19797, A
688	12.2	67.8	71	4	US-09-861-687-15	Sequence 15, Appl	761	12.2	67.8	330	4	US-08-921-976-14872	Sequence 14872, A
689	12.2	67.8	78	1	US-08-400-256-11	Sequence 11, Appl	762	12.2	67.8	338	4	US-09-270-767-8732	Sequence 8732, Ap
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691	12.2	67.8	79	3	US-08-932-082-12	Sequence 12, Appl	764	12.2	67.8	339	4	US-09-543-681A-89	Sequence 89, Appl
692	12.2	67.8	79	4	US-09-861-687-12	Sequence 12, Appl	765	12.2	67.8	345	4	US-09-513-999C-3210	Sequence 3210, Ap
693	12.2	67.8	82	3	US-08-932-082-26	Sequence 26, Appl	766	12.2	67.8	354	4	US-09-513-999C-9308	Sequence 9308, Ap
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695	12.2	67.8	85	3	US-08-932-082-14	Sequence 14, Appl	768	12.2	67.8	360	3	US-09-171-945-10	Sequence 10, Appl
696	12.2	67.8	85	3	US-08-932-082-25	Sequence 25, Appl	769	12.2	67.8	360	3	5486462-7	Patent No. 5486462
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698	12.2	67.8	85	4	US-09-861-687-25	Sequence 25, Appl	771	12.2	67.8	372	1	US-08-780-571-40	Sequence 40, Appl
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700	12.2	67.8	105	4	US-09-513-999C-20252	Sequence 20252, A	773	12.2	67.8	382	3	US-09-103-875-35	Sequence 35, Appl
701	12.2	67.8	110	1	US-08-400-256-3	Sequence 3, Appl	774	12.2	67.8	387	4	US-09-134-000C-485	Sequence 485, App
702	12.2	67.8	110	1	US-08-400-256-7	Sequence 7, Appl	775	12.2	67.8	387	4	US-09-621-976-9357	Sequence 9357, Ap
703	12.2	67.8	110	3	US-08-975-365-3	Sequence 3, Appl	776	12.2	67.8	385	4	US-09-513-999C-1564	Sequence 1564, Ap
704	12.2	67.8	110	3	US-08-975-365-7	Sequence 7, Appl	777	12.2	67.8	386	4	US-09-640-171-148	Sequence 148, App
705	12.2	67.8	117	1	US-08-403-762A-94	Sequence 94, Appl	778	12.2	67.8	396	4	US-09-713-550-148	Sequence 148, App
706	12.2	67.8	121	4	US-09-513-999C-13665	Sequence 13665, A	779	12.2	67.8	396	4	US-09-825-294-148	Sequence 148, App
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832	12.2	67.8	502	4	US-09-686-631-1	Sequence 1, Appli	Sequence 1, Appli	774	4	US-09-107-532A-282	Sequence 282, App
833	12.2	67.8	506	4	US-09-621-976-3351	Sequence 3351, Ap	Sequence 3351, Ap	779	4	US-09-205-258-201	Sequence 201, App
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840	12.2	67.8	523	1	US-08-400-256-41	Sequence 41, Appl	Sequence 41, Appl	795	4	US-09-248-796A-5663	Sequence 5663, Ap
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878	12.2	67.8	594	4	US-09-669-751-239	Sequence 239, App	Sequence 239, App	1128	4	US-09-410-464-7	Sequence 7, Appli
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## ALIGNMENTS

RESULT 1  
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; Sequence 3060, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 3060  
; LENGTH: 1122  
; TYPE: DNA  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-3060

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Best Local Similarity 94.4%; Pred. No. 24;  
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Db 764 ATGCTTGGTACTTGTCTG 781

RESULT 2  
US-09-270-767-31007/c  
; Sequence 31007, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 31007  
; LENGTH: 130  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-31007

Query Match 82.2%; Score 14.8; DB 4; Length 130;  
Best Local Similarity 88.9%; Pred. No. 1.3e+02;  
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Db 30 ATGCTTGGTACTTGGCTG 13

RESULT 3  
US-09-489-039A-3174/c  
; Sequence 3174, Application US/09489039A  
; Patent No. 6810836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 3174  
; LENGTH: 192  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-3174

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Best Local Similarity 88.9%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 43 ATGCTTGGTACTTGGCTG 26

RESULT 4  
US-09-669-751-67  
; Sequence 67, Application US/09669751  
; Patent No. 6551575  
; GENERAL INFORMATION:  
; APPLICANT: Greenspan, Ralph J.  
; TITLE OF INVENTION: Methods for Identifying Compounds for  
; TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to  
; FILE REFERENCE: Balance and the Perception of Gravity  
; CURRENT APPLICATION NUMBER: US/09/669,751  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 60/168,579  
; PRIOR FILING DATE: 1999-12-02  
; NUMBER OF SEQ ID NOS: 261  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 67  
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; TYPE: DNA  
; ORGANISM: Drosophila  
US-09-669-751-67

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Best Local Similarity 88.9%; Pred. No. 1.5e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGCTTGGTACTTGGCTG 18  
Db 383 ATGCTTGGTACTTGGCTG 400

RESULT 5  
US-09-134-001C-307  
; Sequence 307, Application US/09134001C

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; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 307
; LENGTH: 1116
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-307

Query Match      82.2%; Score 14.8; DB 3; Length 1116;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 6
US-09-543-681A-1863
; Sequence 1863, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 1863
; LENGTH: 1242
; TYPE: DNA
; ORGANISM: Proteus mirabilis
; US-09-543-681A-1863

Query Match      82.2%; Score 14.8; DB 4; Length 1242;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ATGCTTGGTACTTGGCTG 18
      |||||
Db      455 ATGCTTGGTCTTGGCTG 472

RESULT 7
US-09-976-594-515/c
; Sequence 515, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 515
```

```
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 228678.1
; US-09-976-594-515

Query Match      82.2%; Score 14.8; DB 4; Length 1467;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ATGCTTGGTACTTGGCTG 18
      |||||
Db      1235 AAGGTGGTACTTGGCTG 1218

RESULT 8
US-09-540-236-1681
; Sequence 1681, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Brston et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 1681
; LENGTH: 2094
; TYPE: DNA
; ORGANISM: M.catarrhalis
; US-09-540-236-1681

Query Match      82.2%; Score 14.8; DB 4; Length 2094;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ATGCTTGGTACTTGGCTG 18
      |||||
Db      677 ATGCTTGGTCTTGGATG 694

RESULT 9
US-09-270-767-14769/c
; Sequence 14769, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14769
; LENGTH: 2138
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; US-09-270-767-14769

Query Match      82.2%; Score 14.8; DB 4; Length 2138;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ATGCTTGGTACTTGGCTG 18
      |||||
Db      30 ATGCTTGGTACTTGGCTG 13

RESULT 10
US-09-596-002-40/c
```

```
; Sequence 40, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert, E.
; APPLICANT: Patterson, Chandra
; APPLICANT: Berg, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: PH-0008-4 US
; CURRENT APPLICATION NUMBER: US/09/596,002
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/140,121
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 40
; LENGTH: 119211
; TYPE: DNA
; ORGANISM: M. catarrhalis
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte template ID No. 6632636 40
; PUBLICATION INFORMATION:
US-09-596-002-40

Query Match      82.2%; Score 14.8; DB 4; Length 119211;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTTGCGTG 18
    |||||
Db 40053 ATGCTTGCTACTTGCGTG 40036

RESULT 11
US-09-270-767-3838/c
; Sequence 3838, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3838
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-3838

Query Match      80.0%; Score 14.4; DB 4; Length 499;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCTTGGTACTTGCGTG 18
    |||||
Db 87 GATTGGTACTTGCGTG 72

RESULT 12
US-09-270-767-19120/c
; Sequence 19120, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19120
```

```
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-19120

Query Match      80.0%; Score 14.4; DB 4; Length 499;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCTTGGTACTTGCGTG 18
    |||||
Db 87 GATTGGTACTTGCGTG 72

RESULT 13
US-09-540-236-444/c
; Sequence 444, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; FILE REFERENCE: 2709 2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 444
; LENGTH: 831
; TYPE: DNA
; ORGANISM: M. catarrhalis
US-09-540-236-444

Query Match      80.0%; Score 14.4; DB 4; Length 831;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCTTGGTACTTGCGT 17
    |||||
Db 120 TGCTTGGTACTTGCGT 105

RESULT 14
US-09-270-767-11600/c
; Sequence 11600, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11600
; LENGTH: 1750
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-11600

Query Match      80.0%; Score 14.4; DB 4; Length 1750;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTTGCG 16
    |||||
Db 1086 ATGCTTGCTACTTGCG 1071

RESULT 15
US-09-614-221A-385
; Sequence 385, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
```



; APPLICANT: Karunanandaa, Balasulojini  
; APPLICANT: Yu, Jaehyuk  
; APPLICANT: Kishore, Ganesh M.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED  
; FILE REFERENCE: 16516.075  
; CURRENT APPLICATION NUMBER: US/09/614,221A  
; CURRENT FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/142,981  
; PRIOR FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 626  
; SEQ ID NO 385  
; LENGTH: 1875  
; TYPE: DNA  
; ORGANISM: Saccharomyces cerevisiae  
US-09-614-221A-385

Query Match 80.0%; Score 14.4; DB 4; Length 1875;  
Best Local Similarity 93.8%; Pred. No. 2.7e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGCTACTGGC 16  
|||||  
Db 1172 ATGCTTGCTACTGGC 1187

RESULT 16  
US-09-799-451-872/c  
; Sequence 872, Application US/09799451  
; Patent No. 6783969  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Zhou, Ping  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Zhang, Jie  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Ma, Yunqing  
; APPLICANT: Yamazaki, Victoria  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Ghosh, Reena  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and  
; FILE REFERENCE: 803  
; CURRENT APPLICATION NUMBER: US/09/799,451  
; CURRENT FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 948  
; SOFTWARE: Pf\_Fl\_genes Version 2.0  
; SEQ ID NO 872  
; LENGTH: 2456  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (72)...(1829)  
US-09-799-451-872

Query Match 80.0%; Score 14.4; DB 4; Length 2496;  
Best Local Similarity 93.8%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGCTTGCTACTGGCT 17  
|||||  
Db 2393 TGCTTGCTACTGGCT 2378

RESULT 17  
US-09-614-221A-353  
; Sequence 353, Application US/09614221A  
; Patent No. 6723837  
; GENERAL INFORMATION:  
; APPLICANT: Karunanandaa, Balasulojini  
; APPLICANT: Yu, Jaehyuk  
; APPLICANT: Kishore, Ganesh M.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED  
; FILE REFERENCE: 16516.075  
; CURRENT APPLICATION NUMBER: US/09/614,221A  
; CURRENT FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/142,981  
; PRIOR FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 626  
; SEQ ID NO 353  
; LENGTH: 3834  
; TYPE: DNA  
; ORGANISM: Saccharomyces cerevisiae  
US-09-614-221A-353

Query Match 80.0%; Score 14.4; DB 4; Length 3834;  
Best Local Similarity 93.8%; Pred. No. 2.9e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGCTACTGGC 16  
|||||  
Db 3131 ATGCTTGCTACTGGC 3146

RESULT 18  
US-09-614-221A-536  
; Sequence 536, Application US/09614221A  
; Patent No. 6723837  
; GENERAL INFORMATION:  
; APPLICANT: Karunanandaa, Balasulojini  
; APPLICANT: Yu, Jaehyuk  
; APPLICANT: Kishore, Ganesh M.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED  
; FILE REFERENCE: 16516.075  
; CURRENT APPLICATION NUMBER: US/09/614,221A  
; CURRENT FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/142,981  
; PRIOR FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 626  
; SEQ ID NO 536  
; LENGTH: 5580  
; TYPE: DNA  
; ORGANISM: Saccharomyces cerevisiae  
US-09-614-221A-536

Query Match 80.0%; Score 14.4; DB 4; Length 5580;  
Best Local Similarity 93.8%; Pred. No. 3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGCTACTGGC 16  
|||||  
Db 4880 ATGCTTGCTACTGGC 4895

RESULT 19  
US-09-596-002-30/c  
; Sequence 30, Application US/09596002  
; Patent No. 6632636  
; GENERAL INFORMATION:  
; APPLICANT: Lagace, Robert, E.  
; APPLICANT: Patterson, Chandra  
; APPLICANT: Berg, Kim, L.  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME  
; FILE REFERENCE: PM-0008-4 US

```
; CURRENT APPLICATION NUMBER: US/09/596,002
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/140,121
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 30
; LENGTH: 58909
; TYPE: DNA
; ORGANISM: M. catarrhalis
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte template ID No. 6632636 30
; PUBLICATION INFORMATION:
US-09-596-002-30

Query Match      80.0%; Score 14.4; DB 4; Length 58909;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 TGCTTGACTTGCGT 17
Db      18646 TGCTTGACTTGCGT 18631

RESULT 20
US-09-388-743-28
; Sequence 28, Application US/09388743
; Patent No. 6423886
; GENERAL INFORMATION:
; APPLICANT: Singletary, George
; APPLICANT: Zhou, Lan
; TITLE OF INVENTION: No. 6423886el Starch Synthase Polynucleotides and Their
; TITLE OF INVENTION: Use in the Production of New Starches
; FILE REFERENCE: 1144
; CURRENT APPLICATION NUMBER: US/09/388,743
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Typha latifolia
US-09-388-743-28

Query Match      77.8%; Score 14; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 TTGGTACTTGCGT 18
Db      7 TTGGTACTTGCGT 20

RESULT 21
US-10-044-543-28
; Sequence 28, Application US/10044543
; Patent No. 6734341
; GENERAL INFORMATION:
; APPLICANT: Singletary, George
; APPLICANT: Zhou, Lan
; TITLE OF INVENTION: No. 6734341el Starch Synthase Polynucleotides
; TITLE OF INVENTION: and Their Use in the Production of New Starches
; FILE REFERENCE: 1144D
; CURRENT APPLICATION NUMBER: US/10/044,543
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 09/388,743
; PRIOR FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 24
; TYPE: DNA

; ORGANISM: Typha latifolia
US-10-044-543-28

Query Match      77.8%; Score 14; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 TTGGTACTTGCGT 18
Db      7 TTGGTACTTGCGT 20

RESULT 22
US-09-614-221A-489/c
; Sequence 489, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
; APPLICANT: Karunanandaa, Balasulojini
; APPLICANT: Yu, Jaenyuk
; APPLICANT: Kishore, Ganesh M.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
; TITLE OF INVENTION: WITH STEROL SYNTHESIS AND METABOLISM
; FILE REFERENCE: 16516.075
; CURRENT APPLICATION NUMBER: US/09/614,221A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/142,981
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 626
; SEQ ID NO 489
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-614-221A-489

Query Match      77.8%; Score 14; DB 4; Length 573;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GCTTGCTACTTGCG 16
Db      275 GCTTGCTACTTGCG 262

RESULT 23
US-09-270-767-10413
; Sequence 10413, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10413
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-10413

Query Match      77.8%; Score 14; DB 4; Length 678;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 TTGGTACTTGCGT 18
Db      301 TTGGTACTTGCGT 314

RESULT 24
US-08-581-148C-13/c
; Sequence 13, Application US/08581148C
```

; Patent No. 6060644  
; GENERAL INFORMATION:  
; APPLICANT: Schnable, Patrick S.  
; APPLICANT: Robertson, Donald S.  
; APPLICANT: Hansen, Joel D.  
; APPLICANT: Nikolau, Basil J.  
; APPLICANT: Xu, Xiaojie  
; APPLICANT: Xia, Yiji  
; TITLE OF INVENTION: ISOLATION AND USE OF CUTICULAR LIPID  
; NUMBER OF INVENTION: GENES  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.  
; STREET: Two Prudential Plaza, Suite 4900  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: US  
; ZIP: 60601-6780  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/581,148C  
; FILING DATE: 29-DEC-1995  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lacher, Carol  
; REGISTRATION NUMBER: 35243  
; REFERENCE/DOCKET NUMBER: 71380  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 616-5600  
; TELEFAX: (312) 616-5700  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1935 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 3..1784  
; US-08-581-148C-13  
  
Query Match 77.8%; Score 14; DB 3; Length 1935;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 TGCTTGCTACTTGG 15  
Db 1427 TGCTTGCTACTTGG 1414  
|||||  
  
RESULT 25  
US-09-388-743-25/c  
; Sequence 25, Application US/09388743  
; Patent No. 6423886  
; GENERAL INFORMATION:  
; APPLICANT: Singletary, George  
; APPLICANT: Zhou, Lan  
; TITLE OF INVENTION: No. 6423886el Starch Synthase Polynucleotides and Their  
; FILE REFERENCE: 1144  
; CURRENT FILING DATE: 1999-09-02  
; CURRENT APPLICATION NUMBER: US/09/388,743  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 2418  
; TYPE: DNA  
; ORGANISM: Typha latifolia

; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(2418)  
; US-09-388-743-25  
  
Query Match 77.8%; Score 14; DB 4; Length 2418;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 TTGTTACTTGGCTG 18  
Db 2148 TTGTTACTTGGCTG 2135  
|||||  
  
RESULT 26  
US-10-044-543-25/c  
; Sequence 25, Application US/10044543  
; Patent No. 6734341  
; GENERAL INFORMATION:  
; APPLICANT: Singletary, George  
; APPLICANT: Zhou, Lan  
; TITLE OF INVENTION: No. 6734341el Starch Synthase Polynucleotides  
; TITLE OF INVENTION: and Their Use in the Production of New Starches  
; FILE REFERENCE: 1144D  
; CURRENT APPLICATION NUMBER: US/10/044,543  
; CURRENT FILING DATE: 2002-01-11  
; PRIOR APPLICATION NUMBER: 09/388,743  
; PRIOR FILING DATE: 1999-09-02  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 2418  
; TYPE: DNA  
; ORGANISM: Typha latifolia  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(2418)  
; US-10-044-543-25  
  
Query Match 77.8%; Score 14; DB 4; Length 2418;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 TTGTTACTTGGCTG 18  
Db 2148 TTGTTACTTGGCTG 2135  
|||||  
  
RESULT 27  
US-07-627-323B-7/c  
; Sequence 7, Application US/07627323B  
; Patent No. 5197973  
; GENERAL INFORMATION:  
; APPLICANT: Pang, Roy H.L.  
; APPLICANT: Cohen, Charles M.  
; APPLICANT: Keck, Peter C.  
; TITLE OF INVENTION: Synthetic Bioadhesive  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Creative Biomolecules  
; STREET: 35 South Street  
; CITY: Hopkinton  
; STATE: MA  
; COUNTRY: U.S.A.  
; ZIP: 01748  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/627,323B  
; FILING DATE: 19901214

```

; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 3..59
; US-07-988-754-7

Query Match          76.7%; Score 13.8; DB 1; Length 63;
Best Local Similarity 88.2%; Pred. NO. 3.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2  TCCTTGGTACTTGGCTG 18
          ||||| ||||| |||||
Db      29  TCCTTGGTACTTAGCTG 13

RESULT 29
US-07-627-323-7/c
Sequence 7, Application US/08100691

```

```

: GENERAL INFORMATION:
: APPLICANT: Edgelson, Richard L.
: APPLICANT: Gasparro, Francis P.
: TITLE OF INVENTION: Cellular Vaccine and Methods of Use for
: TITLE OF INVENTION: the Treatment of Solid Tumor Malignancies
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
:

```

```

CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,691
FILING DATE: 19930730
CLASSIFICATION: 424
PRIORITY:
APPLICATION DATA:
APPLICATION NUMBER: US 07/977672
FILING DATE: 18-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: Y0060/7005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 base pairs
TYPE: NUCLEIC ACID
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-07-627-323-7

Query Watch 76.7%; Score 13.8; DB 1; Length 63;
Best Local Similarity 88.2%; Pred. No. 3.8e-02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGC TTGGTACTTGGCTG 18
Db 29 TGC TTGTACTTAGCTG 13

RESULT 30

```

US-07-627-323B-11/c  
; Sequence 11, Application US/07627323B  
; Patent No. 5197973  
; GENERAL INFORMATION:  
; APPLICANT: Pang, Roy H.L.  
; APPLICANT: Cohen, Charles M.  
; APPLICANT: Keck, Peter C.  
; TITLE OF INVENTION: Synthetic Bioadhesive  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Creative Biomolecules  
; STREET: 35 South Street  
; CITY: Hopkinton  
; STATE: MA  
; COUNTRY: U.S.A.  
; ZIP: 01748  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/627,323B  
; FILING DATE: 19901214  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G.  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: CRP-046  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (508) 435-9001  
; TELEFAX: (508) 435-6951  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 105 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 3..101  
US-07-627-323B-11

Query Match 76.7%; Score 13.8; DB 1; Length 105;  
Best Local Similarity 88.2%; Pred. No. 4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCTTGGTACTTGCTG 18  
|||||  
Db 29 TGCITTTGACTTAGCTG 13

RESULT 31  
US-07-988-754-11/c  
; Sequence 11, Application US/07988754  
; Patent No. 5374431  
; GENERAL INFORMATION:  
; APPLICANT: Pang, Roy H.L.  
; APPLICANT: Cohen, Charles M.  
; APPLICANT: Keck, Peter C.  
; TITLE OF INVENTION: Synthetic Bioadhesive  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Creative Biomolecules  
; STREET: 35 South Street  
; CITY: Hopkinton  
; STATE: MA  
; COUNTRY: U.S.A.  
; ZIP: 01748

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/988,754  
; FILING DATE: 19921210  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/627,323  
; FILING DATE: 14-DEC-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G.  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: CRP-046  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (508) 435-9001  
; TELEFAX: (508) 435-6951  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 105 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 3..101  
US-07-988-754-11

Query Match 76.7%; Score 13.8; DB 1; Length 105;  
Best Local Similarity 88.2%; Pred. No. 4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCTTGGTACTTGCTG 18  
|||||  
Db 29 TGCITTTGACTTAGCTG 13

RESULT 32  
US-09-134-000C-405  
; Sequence 405, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 405  
; LENGTH: 183  
; TYPE: DNA  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-405

Query Match 76.7%; Score 13.8; DB 4; Length 183;  
Best Local Similarity 88.2%; Pred. No. 4.2e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCTTGGTACTTGCT 17  
|||||  
Db 38 ATGCTTGTACTTGTT 54

```
RESULT 33
US-09-360-376-26
; Sequence 26, Application US/09360376
; Patent No. 6495739
; GENERAL INFORMATION:
; APPLICANT: Lassner, Michael
; APPLICANT: Ruzinsky, Diane
; TITLE OF INVENTION: PLANT PHOSPHATIDIC ACID PHOSPHATASES
; FILE REFERENCE: 17026/01/US
; CURRENT APPLICATION NUMBER: US/09/360,376
; CURRENT FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: US 09/122,315
; PRIOR FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Zea mays
US-09-360-376-26

Query Match 76.7%; Score 13.8; DB 4; Length 256;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCTTGGTACTGGCTG 18
Db 208 TGCATGGTACTAGCTG 224

RESULT 34
US-09-360-376-24
; Sequence 24, Application US/09360376
; Patent No. 6495739
; GENERAL INFORMATION:
; APPLICANT: Lassner, Michael
; APPLICANT: Ruzinsky, Diane
; TITLE OF INVENTION: PLANT PHOSPHATIDIC ACID PHOSPHATASES
; FILE REFERENCE: 17026/01/US
; CURRENT APPLICATION NUMBER: US/09/360,376
; CURRENT FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: US 09/122,315
; PRIOR FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 259
; TYPE: DNA
; ORGANISM: Zea mays
; NAME/KEY: misc feature
; LOCATION: (1)..(259)
; OTHER INFORMATION: n = A, T, C, or G
US-09-360-376-24

Query Match 76.7%; Score 13.8; DB 4; Length 259;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCTTGGTACTGGCTG 18
Db 186 TGCATGGTACTAGCTG 202

RESULT 35
US-09-360-376-25
; Sequence 25, Application US/09360376
; Patent No. 6495739
; GENERAL INFORMATION:
; APPLICANT: Lassner, Michael
; APPLICANT: Ruzinsky, Diane
; TITLE OF INVENTION: PLANT PHOSPHATIDIC ACID PHOSPHATASES
; FILE REFERENCE: 17026/01/US
; CURRENT APPLICATION NUMBER: US/09/360,376
; CURRENT FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: US 09/122,315
; PRIOR FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Zea mays
US-09-360-376-25

Query Match 76.7%; Score 13.8; DB 4; Length 262;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCTTGGTACTGGCTG 18
Db 45 TGCATGGTACTAGCTG 61

RESULT 36
US-09-360-376-18
; Sequence 18, Application US/09360376
; Patent No. 6495739
; GENERAL INFORMATION:
; APPLICANT: Lassner, Michael
; APPLICANT: Ruzinsky, Diane
; TITLE OF INVENTION: PLANT PHOSPHATIDIC ACID PHOSPHATASES
; FILE REFERENCE: 17026/01/US
; CURRENT APPLICATION NUMBER: US/09/360,376
; CURRENT FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: US 09/122,315
; PRIOR FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 267
; TYPE: DNA
; ORGANISM: Zea mays
; NAME/KEY: misc feature
; LOCATION: (1)..(267)
; OTHER INFORMATION: n = A, T, C, or G
US-09-360-376-18

Query Match 76.7%; Score 13.8; DB 4; Length 267;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCTTGGTACTGGCTG 18
Db 202 TGCATGGTACTAGCTG 218

RESULT 37
US-09-313-294A-1839
; Sequence 1839, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Laigudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 1839
; LENGTH: 274
; TYPE: DNA
; ORGANISM: Zea mays
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; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700551611H1
US-09-313-294A-1839

Query Match      76.7%; Score 13.8; DB 4; Length 274;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCTTGGTACTTGGCTG 18
Db 72 TGCATGGTACTTAGCTG 88

RESULT 38
US-09-360-376-31
; Sequence 31, Application US/09360376
; Patent No. 6495739
; GENERAL INFORMATION:
; APPLICANT: Lassner, Michael
; APPLICANT: Ruzinsky, Diane
; TITLE OF INVENTION: PLANT PHOSPHATIDIC ACID PHOSPHATASES
; FILE REFERENCE: 17026/01/US
; CURRENT APPLICATION NUMBER: US/09/360,376
; CURRENT FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: US 09/122,315
; PRIOR FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 281
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(281)
; OTHER INFORMATION: n = A, T, C, or G
US-09-360-376-31

Query Match      76.7%; Score 13.8; DB 4; Length 281;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCTTGGTACTTGGCTG 18
Db 63 TGCATGGTACTTAGCTG 79

RESULT 39
US-09-360-376-27
; Sequence 27, Application US/09360376
; Patent No. 6495739
; GENERAL INFORMATION:
; APPLICANT: Lassner, Michael
; APPLICANT: Ruzinsky, Diane
; TITLE OF INVENTION: PLANT PHOSPHATIDIC ACID PHOSPHATASES
; FILE REFERENCE: 17026/01/US
; CURRENT APPLICATION NUMBER: US/09/360,376
; CURRENT FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: US 09/122,315
; PRIOR FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 289
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(289)
; OTHER INFORMATION: n = A, T, C, or G
US-09-360-376-27

Query Match      76.7%; Score 13.8; DB 4; Length 289;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCTTGGTACTTGGCTG 18
Db 210 TGCATGGTACTTAGCTG 226

RESULT 40
US-09-313-294A-6051/c
; Sequence 6051, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Ialgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 6051
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700351145H1
; NAME/KEY: unsure
; LOCATION: 109
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-6051

Query Match      76.7%; Score 13.8; DB 4; Length 291;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCTTGGTACTTGGCTG 18
Db 267 TGCITGGTAAATGGCTG 251

RESULT 41
US-09-360-376-29
; Sequence 29, Application US/09360376
; Patent No. 6495739
; GENERAL INFORMATION:
; APPLICANT: Lassner, Michael
; APPLICANT: Ruzinsky, Diane
; TITLE OF INVENTION: PLANT PHOSPHATIDIC ACID PHOSPHATASES
; FILE REFERENCE: 17026/01/US
; CURRENT APPLICATION NUMBER: US/09/360,376
; CURRENT FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: US 09/122,315
; PRIOR FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Zea mays
US-09-360-376-29

Query Match      76.7%; Score 13.8; DB 4; Length 297;
Best Local Similarity 88.2%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCTTGGTACTTGGCTG 18
Db 63 TGCATGGTACTTAGCTG 79
```

RESULT 42  
US-09-702-705-269  
; Sequence 269, Application US/09702705  
; Patent No. 6504010  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Lodes, Michael A.  
; APPLICANT: Fanger, Gary  
; APPLICANT: Vedrick, Tom  
; APPLICANT: Carter, Darrick  
; APPLICANT: Retter, Marc  
; APPLICANT: Mannion, Jane  
; APPLICANT: Fan, Liqun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.478C14  
; CURRENT APPLICATION NUMBER: US/09/702,705  
; CURRENT FILING DATE: 2000-10-30  
; NUMBER OF SEQ ID NOS: 1833  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 269  
; LENGTH: 325  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-702-705-269

Query Match 76.7%; Score 13.8; DB 4; Length 325;  
Best Local Similarity 88.2%; Pred. No. 4.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 ATGCTTGGTACTGGCT 17  
Db 115 ATGCTTGGTAATTGGTT 131

RESULT 43  
US-09-736-457-269  
; Sequence 269, Application US/09736457  
; Patent No. 8509448  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Lodes, Michael A.  
; APPLICANT: Fanger, Gary  
; APPLICANT: Vedrick, Tom  
; APPLICANT: Carter, Darrick  
; APPLICANT: Retter, Marc  
; APPLICANT: Mannion, Jane  
; APPLICANT: Fan, Liqun  
; APPLICANT: Wang, Aijun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.478C15  
; CURRENT APPLICATION NUMBER: US/09/736,457  
; CURRENT FILING DATE: 2000-12-13  
; NUMBER OF SEQ ID NOS: 1864  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 269  
; LENGTH: 325  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-736-457-269

Query Match 76.7%; Score 13.8; DB 4; Length 325;  
Best Local Similarity 88.2%; Pred. No. 4.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 ATGCTTGGTACTGGCT 17  
Db 115 ATGCTTGGTAATTGGTT 131

RESULT 44  
US-09-614-124B-269  
; Sequence 269, Application US/09614124B  
; Patent No. 6630574  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Lodes, Michael A.  
; APPLICANT: Fanger, Gary  
; APPLICANT: Vedrick, Tom  
; APPLICANT: Carter, Darrick  
; APPLICANT: Retter, Marc  
; APPLICANT: Mannion, Jane  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
; FILE REFERENCE: 210121.478C9  
; CURRENT APPLICATION NUMBER: US/09/614,124B  
; CURRENT FILING DATE: 2001-07-11  
; NUMBER OF SEQ ID NOS: 1668  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 269  
; LENGTH: 325  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-614-124B-269

Query Match 76.7%; Score 13.8; DB 4; Length 325;  
Best Local Similarity 88.2%; Pred. No. 4.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 ATGCTTGGTACTGGCT 17  
Db 115 ATGCTTGGTAATTGGTT 131

RESULT 45  
US-09-671-325-269  
; Sequence 269, Application US/09671325  
; Patent No. 6667154  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Lodes, Michael A.  
; APPLICANT: Fanger, Gary  
; APPLICANT: Vedrick, Tom  
; APPLICANT: Carter, Darrick  
; APPLICANT: Retter, Marc  
; APPLICANT: Mannion, Jane  
; APPLICANT: Fan, Liqun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.478C12  
; CURRENT APPLICATION NUMBER: US/09/671,325  
; CURRENT FILING DATE: 2000-09-26  
; NUMBER OF SEQ ID NOS: 1825  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 269  
; LENGTH: 325  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-671-325-269

Query Match 76.7%; Score 13.8; DB 4; Length 325;  
Best Local Similarity 88.2%; Pred. No. 4.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 ATGCTTGGTACTGGCT 17  
Db 115 ATGCTTGGTAATTGGTT 131

RESULT 46



```
US-09-589-184-269
; Sequence 269, Application US/09589184
; Patent No. 6886447
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C8
; CURRENT APPLICATION NUMBER: US/09/589,184
; CURRENT FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 827
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 269
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-589-184-269

Query Match 76.7%; Score 13.8; DB 4; Length 325;
Best Local Similarity 88.2%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCTTGGTACTGGCT 17
Db 115 ATGCTTGGTAATTGGTT 131

RESULT 47
US-09-658-824-269
; Sequence 269, Application US/09658824
; Patent No. 6746846
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C11
; CURRENT APPLICATION NUMBER: US/09/658,824
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 1788
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 269
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-658-824-269

Query Match 76.7%; Score 13.8; DB 4; Length 325;
Best Local Similarity 88.2%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCTTGGTACTGGCT 17
Db 115 ATGCTTGGTAATTGGTT 131

US-09-513-999C-698/c
; Sequence 698, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: EXPRESSED SEQUENCE TAGS AND ENCODED HUMAN PROTEINS.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
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US-09-621-976-18061/c
; Sequence 18061, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTS AND ENCODED HUMAN PROTEINS.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 18061
; LENGTH: 436
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; ORGANISM: Homo sapiens
US-09-621-976-18061

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Best Local Similarity 88.2%; Pred. No. 4.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 232 ATGCTTGGTAATTGGTT 216

RESULT 50
US-09-513-999C-698/c
; Sequence 698, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: EXPRESSED SEQUENCE TAGS AND ENCODED HUMAN PROTEINS.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
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US-09-360-376-34
; Patent No. 6495739
; GENERAL INFORMATION:
; APPLICANT: Ruzinsky, Diane
; APPLICANT: Ruzinsky, Diane
; TITLE OF INVENTION: PLANT PHOSPHATIDIC ACID PHOSPHATASES
; FILE REFERENCE: 17026/01/US
; CURRENT APPLICATION NUMBER: US/09/360,376
; CURRENT FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: US 09/122,315
; PRIOR FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 34
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: ( )..( )
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US-09-360-376-34

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Best Local Similarity 88.2%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36691
; SOFTWARE: Patent.pm
; SEQ ID NO 698
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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US-09-513-999C-698

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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Title: US-10-050-189A-9

Perfect score: 18

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Scoring table: IDENTITY\_NUC

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Post-processing: Minimum Match 0%

Listing first 1000 summaries

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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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C 172	15.4	85.6	642	6	CA102152	SCAGHR101	246	15.4	85.6	1681	1	AK046675	Mus muscu
C 173	15.4	85.6	642	6	CA102152	SCAGHR101	247	15.4	85.6	1681	1	AK046675	Mus muscu
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C 180	15.4	85.6	642	6	CA102152	SCAGHR101	254	15.4	85.6	1681	1	AK046675	Mus muscu
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C 187	15.4	85.6	642	6	CA102152	SCAGHR101	261	15.4	85.6	1681	1	AK046675	Mus muscu
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C 189	15.4	85.6	642	6	CA102152	SCAGHR101	263	15.4	85.6	1681	1	AK046675	Mus muscu
C 190	15.4	85.6	642	6	CA102152	SCAGHR101	264	15.4	85.6	1681	1	AK046675	Mus muscu
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C 390	15	83.3	644	5	BU689340	UI-CF-EC1	BU689340	UI-CF-EC1	C 463	14.8	82.2	218	8	AQ391064	CITBI-P1-
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C 393	15	83.3	648	7	BB626336	BB626336	BB626336	BB626336	C 466	14.8	82.2	245	6	C78755	Mous
394	15	83.3	648	7	CN662168	A0729G06-	CN662168	A0729G06-	467	14.8	82.2	250	1	AV367633	AV367633
C 395	15	83.3	652	2	BF505807	AT08204.5	BF505807	AT08204.5	468	14.8	82.2	253	1	AV355733	AV355733
C 396	15	83.3	656	7	C0223091	WS01017.B	C0223091	WS01017.B	469	14.8	82.2	256	9	CG526668	OSI103483
397	15	83.3	675	8	CC168860	1156911.9	CC168860	1156911.9	470	14.8	82.2	257	2	AW453556	zeli00986
C 398	15	83.3	680	6	CA504879	RI-M-FJO-	CA504879	RI-M-FJO-	471	14.8	82.2	258	9	CG666753	OSI457549
C 399	15	83.3	681	8	AZ825902	2M0101P16	AZ825902	2M0101P16	472	14.8	82.2	260	7	R52134	Y72203.51
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C 401	15	83.3	692	7	CF534383	UI-M-PYO-	CF534383	UI-M-PYO-	474	14.8	82.2	264	1	AV100873	AV100873
402	15	83.3	694	2	BE866880	601445822	BE866880	601445822	475	14.8	82.2	268	1	AV093192	AV093192
C 403	15	83.3	698	7	CN358584	170006000	CN358584	170006000	476	14.8	82.2	268	2	B2326848	BE2326848
C 404	15	83.3	699	2	BF508850	UI-H-B14-	BF508850	UI-H-B14-	477	14.8	82.2	268	9	CG671551	OSI500795
405	15	83.3	700	9	CE153407	tigr-gss-	CE153407	tigr-gss-	C 478	14.8	82.2	273	8	AZ563638	RPCI-23-2
C 406	15	83.3	719	8	BE278239	OECN62TM	BE278239	OECN62TM	C 479	14.8	82.2	282	6	CA794250	Cac BL-17
407	15	83.3	721	9	CE207484	tigr-gss-	CE207484	tigr-gss-	480	14.8	82.2	283	9	CG587967	OSI238145
408	15	83.3	721	9	CE399248	tigr-gss-	CE399248	tigr-gss-	C 481	14.8	82.2	284	8	AQ005489	CIT-HSP-2
409	15	83.3	728	7	CN203521	Tor3803.G	CN203521	Tor3803.G	C 482	14.8	82.2	284	9	AG195187	Pan trogl
C 410	15	83.3	734	8	BZ728322	OECN62TC	BZ728322	OECN62TC	483	14.8	82.2	285	9	CG515357	OSI70421
C 411	15	83.3	737	2	BF498321	AT1212.5	BF498321	AT1212.5	484	14.8	82.2	288	1	AV150748	AV150748
412	15	83.3	744	1	AV692960	AV692960	AV692960	AV692960	C 485	14.8	82.2	288	8	AZ835082	2M0129B11
C 413	15	83.3	746	9	CV570568	CH240.446	CV570568	CH240.446	486	14.8	82.2	289	1	AV136399	AV136399
414	15	83.3	757	7	CF743720	UI-M-G10-	CF743720	UI-M-G10-	487	14.8	82.2	290	1	AV308034	AV308034
415	15	83.3	758	7	CN358587	170005325	CN358587	170005325	488	14.8	82.2	291	1	AV129268	AV129268
416	15	83.3	758	8	CC336425	OGUBM12TH	CC336425	OGUBM12TH	489	14.8	82.2	293	2	B401742	B401742
417	15	83.3	760	9	CG824952	SOYAE11TH	CG824952	SOYAE11TH	490	14.8	82.2	295	1	AV150007	AV150007
418	15	83.3	767	7	CK781089	UI-M-GV0-	CK781089	UI-M-GV0-	491	14.8	82.2	297	1	AV016302	AV016302
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420	15	83.3	771	7	CN200682	Tor10346	CN200682	Tor10346	493	14.8	82.2	298	1	AV154346	AV154346
421	15	83.3	776	5	BQ185934	UI-E-EJ1-	BQ185934	UI-E-EJ1-	494	14.8	82.2	298	9	CG632260	OSI350119
422	15	83.3	782	4	BG823860	602739529	BG823860	602739529	C 495	14.8	82.2	299	6	CB425475	600478 MA
423	15	83.3	787	2	BF695732	602727142	BF695732	602727142	496	14.8	82.2	302	1	AV135502	AV135502
C 424	15	83.3	787	4	BG65248	H3028H09	BG65248	H3028H09	497	14.8	82.2	302	1	AV154164	AV154164
C 425	15	83.3	789	2	BF502000	AT17604.5	BF502000	AT17604.5	C 498	14.8	82.2	304	1	AZ516655	RPCI-11-3
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C 427	15	83.3	792	9	CG035032	CG035032	CG035032	CG035032	500	14.8	82.2	305	9	CG642809	OSI79609
428	15	83.3	793	5	BU747204	CH3010.B	BU747204	CH3010.B	501	14.8	82.2	306	1	AV153053	AV153053
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430	15	83.3	797	9	CNS009F6	Drosophila	AL053498	Drosophila	503	14.8	82.2	316	4	BG438863	dab19904.
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435	15	83.3	903	2	BE884123	601506070	BE884123	601506070	508	14.8	82.2	334	2	BB012145	BB012145
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437	15	83.3	915	9	CG171322	PUFV45TD	CG171322	PUFV45TD	510	14.8	82.2	344	4	BF559131	UI-R-C1-K
438	15	83.3	918	9	CG192274	PUFV12TB	CG192274	PUFV12TB	511	14.8	82.2	344	4	BG558605	RH22.58
439	15	83.3	934	5	Q9393118	AGENCOURT	Q9393118	AGENCOURT	C 512	14.8	82.2	346	7	CR476029	CR476029
C 440	15	83.3	935	9	CG692365	OGUBM12TV	CG692365	OGUBM12TV	C 513	14.8	82.2	348	3	CNS08TSH	Single re
441	15	83.3	936	2	BF342475	602013983	BF342475	602013983	514	14.8	82.2	348	4	BI065525	pgfin.pko
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C 443	15	83.3	960	4	BI247552	602960003	BI247552	602960003	C 516	14.8	82.2	350	5	BU085756	SnST4a89
C 444	15	83.3	964	1	AL578187	AL578187	AL578187	AL578187	C 517	14.8	82.2	351	8	AZ353938	IM0093H02
445	15	83.3	969	5	Q9631476	AGENCOURT	Q9631476	AGENCOURT	C 518	14.8	82.2	358	5	BY085811	BY085811
446	15	83.3	981	5	EQ721045	AGENCOURT	EQ721045	AGENCOURT	C 519	14.8	82.2	367	4	BG439533	dab18004.
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451	15	83.3	1752	3	AK049551	Mus muscu	AK049551	Mus muscu	524	14.8	82.2	380	9	CG620023	OSI316598
452	15	83.3	2973	3	AK034313	Mus muscu	AK034313	Mus muscu	525	14.8	82.2	383	9	CG627164	OSI336607
453	15	83.3	4355	3	HSMB00159	Homio sapi	AL833819	Homio sapi	526	14.8	82.2	384	6	CA790251	CA790251
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C 456	14.8	82.2	177	2	BE492458	WHE553.BO	BE492458	WHE553.BO	C 529	14.8	82.2	388	1	AA132600	AA132600
457	14.8	82.2	184	1	AV170823	AV170823	AV170823	AV170823	C 530	14.8	82.2	388	9	CG495964	CG495964
458	14.8	82.2	188	1	AJ443379	AJ443379	AJ443379	AJ443379	C 531	14.8	82.2	390	6	CB778448	CB778448
459	14.8	82.2	190	5	BP748324	BP748324	BP748324	BP748324	C 532	14.8	82.2	393	5	BX683491	BX683491
460	14.8	82.2	191	6	CD682990	FJ29a10.Y	CD682990	FJ29a10.Y	C 533	14.8	82.2	395	4	BG346126	BG346126
C 461	14.8	82.2	197	1	AL933306	AL933306	AL933306	AL933306	534	14.8	82.2	396	4	BG234835	AG11189.5
C 462	14.8	82.2	218	4	BG221469	RST41281	BG221469	RST41281	C 535	14.8	82.2	397	1	AI228384	EST225079

536	14.8	82.2	398	6	CB707500	CB707500	ANGNUC:T	603	14.8	82.2	485	7	N47789	N47789	YV93B09.s1
537	14.8	82.2	399	2	AW157919	AW157919	zaz3b06.x	c 610	14.8	82.2	485	9	BX204258	BX204258	Danio rer
538	14.8	82.2	400	8	BZ340811	BZ340811	ic41b10.g	c 611	14.8	82.2	486	2	BF889715	BF889715	289280.MA
539	14.8	82.2	403	5	BU421043	BU421043	603962112	c 612	14.8	82.2	486	8	AQ389845	AQ389845	RPC111-14
540	14.8	82.2	403	7	R52148	R52148	yj72e03.s1	c 613	14.8	82.2	488	2	AW114714	AW114714	rs5306.Y
541	14.8	82.2	404	8	AQ146681	AQ146681	HS 2242.A	c 614	14.8	82.2	489	8	AZ167359	AZ167359	SP 0098.A
542	14.8	82.2	406	8	AZ293926	AZ293926	RPC1-23-1	c 615	14.8	82.2	489	9	CG598149	CG598149	OST262275
543	14.8	82.2	409	7	N94138	N94138	za25h06.r1	c 616	14.8	82.2	490	7	CK444069	CK444069	GQ0015d.B
544	14.8	82.2	410	6	BY653416	BY653416	BY653416	c 617	14.8	82.2	491	1	AI082225	AI082225	ox79e10.X
545	14.8	82.2	413	1	AI989107	AI989107	rs29h10.Y	c 618	14.8	82.2	491	1	AA097009	AA097009	mm52b02.r
546	14.8	82.2	413	8	AQ205975	AQ205975	HS 3236.B	c 619	14.8	82.2	491	7	W29499	W29499	mc02ell.r1
547	14.8	82.2	414	2	BE726047	BE726047	BB726047	c 620	14.8	82.2	491	9	AG204894	AG204894	Pan trogl
548	14.8	82.2	414	2	BE863103	BE863103	UT-M-BHO-	c 621	14.8	82.2	492	9	CG666754	CG666754	OST457550
549	14.8	82.2	414	8	AQ651937	AQ651937	Sheared D	c 622	14.8	82.2	493	8	AZ777853	AZ777853	2M0012G12
550	14.8	82.2	416	1	AI071527	AI071527	UT-R-C1-k	c 623	14.8	82.2	496	6	CD892918	CD892918	G118.132F
551	14.8	82.2	416	2	BE236847	BE236847	145825.HA	c 624	14.8	82.2	497	4	CG670761	CG670761	OST471435
552	14.8	82.2	417	4	BI075609	BI075609	IF1_22.HO	c 625	14.8	82.2	498	8	BG731757	BG731757	dac30d10.
553	14.8	82.2	418	9	CG515335	CG515335	OST69908	c 626	14.8	82.2	498	8	AK430730	AK430730	IM0215F17
554	14.8	82.2	419	8	AQ925053	AQ925053	RPC1-23-3	c 627	14.8	82.2	499	8	CK468603	CK468603	AMF123.HO
555	14.8	82.2	420	1	AV418250	AV418250	AV418250	c 628	14.8	82.2	499	8	BZ377111	BZ377111	ie77g08.g
556	14.8	82.2	420	5	CB798663	CB798663	ANGNUC:S	c 629	14.8	82.2	501	7	CK440601	CK440601	GQ0026b.T
557	14.8	82.2	421	2	BE673110	BE673110	BB673110	c 630	14.8	82.2	502	9	CG650803	CG650803	OST409370
558	14.8	82.2	424	2	BB810711	BB810711	BB810711	c 631	14.8	82.2	503	1	AA655856	AA655856	vs22c05.r
559	14.8	82.2	425	8	AQ189185	AQ189185	HS 3165.B	c 632	14.8	82.2	503	7	CN548062	CN548062	EST 15700
560	14.8	82.2	427	8	AQ357980	AQ357980	HS 2254.B	c 633	14.8	82.2	504	9	CG608357	CG608357	OST288417
561	14.8	82.2	429	7	CN913321	CN913321	030107ABM	c 634	14.8	82.2	504	9	CG600652	CG600652	OST270530
562	14.8	82.2	429	9	CG967160	CG967160	MBEHN23TR	c 635	14.8	82.2	505	5	BQ385503	BQ385503	NISC.mn12
563	14.8	82.2	430	1	AA024657	AA024657	z877g08.s	c 636	14.8	82.2	505	6	CB360465	CB360465	ZF001-P00
564	14.8	82.2	433	8	AZ154875	AZ154875	SP 0032.A	c 637	14.8	82.2	505	7	CK440600	CK440600	GQ0026b.B
565	14.8	82.2	434	1	AA074657	AA074657	zm76g03.r1	c 638	14.8	82.2	508	1	AA473352	AA473352	vd45f10.r
566	14.8	82.2	436	2	BE236849	BE236849	145827.MA	c 639	14.8	82.2	508	5	BQ630621	BQ630621	sap28h05.
567	14.8	82.2	436	6	CB782115	CB782115	ANGNUC:N	c 640	14.8	82.2	508	9	CG665293	CG665293	OST453426
568	14.8	82.2	439	8	AQ277937	AQ277937	CITBI-E1-	c 641	14.8	82.2	509	9	CG609990	CG609990	OST292110
569	14.8	82.2	440	1	AI058424	AI058424	UI-R-C1-k	c 642	14.8	82.2	510	7	BF558782	BF558782	UI-R-A1-d
570	14.8	82.2	441	7	CO299222	CO299222	EX174824.	c 643	14.8	82.2	510	7	CR548228	CR548228	DKF2p459M
571	14.8	82.2	444	5	BY211231	BY211231	BZ211231	c 644	14.8	82.2	510	9	CG650827	CG650827	OST409574
572	14.8	82.2	445	7	CK890765	CK890765	SGP163024	c 645	14.8	82.2	511	2	AA9337859	AA9337859	QV3-DT004
573	14.8	82.2	445	7	CO189101	CO189101	EX043026.	c 646	14.8	82.2	512	1	AA131530	AA131530	z133d07.s
574	14.8	82.2	445	9	CG669983	CG669983	OST467778	c 647	14.8	82.2	512	9	CG646283	CG646283	OST392078
575	14.8	82.2	449	7	CF609504	CF609504	INF1001.0	c 648	14.8	82.2	513	7	CN548311	CN548311	EST 15949
576	14.8	82.2	449	9	CG500874	CG500874	OST44047	c 649	14.8	82.2	513	9	CG663815	CG663815	OST449482
577	14.8	82.2	450	1	AV712273	AV712273	AV712273	c 650	14.8	82.2	514	1	AU205105	AU205105	OST405105
578	14.8	82.2	450	2	AW347478	AW347478	UI-R-BUOp	c 651	14.8	82.2	514	5	BQ385375	BQ385375	NISC.mn11
579	14.8	82.2	450	5	BY566571	BY566571	BY566571	c 652	14.8	82.2	514	8	AQ082803	AQ082803	RPC111-54
580	14.8	82.2	451	1	AA245517	AA245517	my50c02.r	c 653	14.8	82.2	515	9	AG253381	AG253381	Lotus cor
581	14.8	82.2	452	5	BP643320	BP643320	BP643320	c 654	14.8	82.2	517	8	AZ214593	AZ214593	Sheared D
582	14.8	82.2	453	5	BQ697351	BQ697351	NXPV 053	c 655	14.8	82.2	517	8	AQ429436	AQ429436	CITBI-E1-
583	14.8	82.2	453	5	BY298726	BY298726	BY298726	c 656	14.8	82.2	519	4	BI315449	BI315449	daf86g04.
584	14.8	82.2	455	8	AZ193174	AZ193174	SG1039.A	c 657	14.8	82.2	520	9	CG322022	CG322022	OGWL87TV
585	14.8	82.2	455	9	CG657697	CG657697	OST432570	c 658	14.8	82.2	521	9	CB833145	CB833145	tiGr-g88-
586	14.8	82.2	459	6	CD194453	CD194453	MS1-0086U	c 659	14.8	82.2	523	7	CO420821	CO420821	GGE2HC02
587	14.8	82.2	463	4	BI713962	BI713962	ic87g12.x	c 660	14.8	82.2	524	1	AA895851	AA895851	vy35a02.r
588	14.8	82.2	463	2	BE624577	BE624577	uu23h02.Y	c 661	14.8	82.2	524	8	AZ158069	AZ158069	SP 0060.A
589	14.8	82.2	465	6	CB714662	CB714662	ANGNUC:M	c 662	14.8	82.2	526	1	AI411623	AI411623	EST239917
590	14.8	82.2	466	6	AL921081	AL921081	AL921081	c 663	14.8	82.2	526	9	CG185112	CG185112	PUIET27TD
591	14.8	82.2	467	1	AZ154355	AZ154355	SP 0035.A	c 664	14.8	82.2	526	9	CG636653	CG636653	OST361496
592	14.8	82.2	470	8	BG731452	BG731452	d8c25d07.	c 665	14.8	82.2	527	5	BP034916	BP034916	BP034916
593	14.8	82.2	472	5	BY240962	BY240962	BY240962	c 666	14.8	82.2	527	5	BQ385130	BQ385130	NISC.mn10
594	14.8	82.2	474	8	AQ121922	AQ121922	HS 3090.A	c 667	14.8	82.2	528	9	CG836643	CG836643	OST361488
595	14.8	82.2	475	5	BP043577	BP043577	BP043577	c 668	14.8	82.2	529	2	BF567772	BF567772	UI-R-BUO-
596	14.8	82.2	475	5	BU340988	BU340988	603520703	c 669	14.8	82.2	530	9	CG647403	CG647403	OST396366
597	14.8	82.2	477	8	AZ149978	AZ149978	SP 0037.B	c 670	14.8	82.2	531	1	AL042183	AL042183	DKF2p434F
598	14.8	82.2	478	8	AQ014033	AQ014033	CG14033	c 671	14.8	82.2	531	5	BU369930	BU369930	603596812
599	14.8	82.2	480	7	CK437856	CK437856	CG0041.TB	c 672	14.8	82.2	531	5	BU405201	BU405201	603483882
600	14.8	82.2	481	1	KA913851	KA913851	CG100477	c 673	14.8	82.2	531	8	AQ167523	AQ167523	SP 0098.B
601	14.8	82.2	481	7	AA915256	AA915256	vz12e08.r	c 674	14.8	82.2	531	8	AQ710675	AQ710675	HS-5344.A
602	14.8	82.2	481	5	BU276538	BU276538	603603086	c 675	14.8	82.2	532	7	N47723	N47723	YV92H09.s1
603	14.8	82.2	483	1	AT263421	AT263421	g106e02.x	c 676	14.8	82.2	533	5	BP040464	BP040464	BP040464
604	14.8	82.2	483	1	BE697827	BE697827	BE697827	c 677	14.8	82.2	536	2	AW173942	AW173942	f137e07.Y
605	14.8	82.2	483	4	BI449393	BI449393	de27g01.x	c 678	14.8	82.2	536	6	CA625249	CA625249	w11n.pk01
606	14.8	82.2	483	7	CF815502	CF815502	EST692884	c 679	14.8	82.2	536	8	AQ276392	AQ276392	CITBI-E1-
607	14.8	82.2	484	5	BQ781473	BQ781473	UI-R-EF0-	c 680	14.8	82.2	537	7	CN851539	CN851539	020806AAP
608	14.8	82.2	485	7	CF930940	CF930940	CF--05-R-	c 681	14.8	82.2	538	4	BG010618	BG010618	MR3-GN019

682	14.8	82.2	538	9	CG625099	OST329953	C 755	14.8	82.2	630	7	CN228543	RJB092B02
683	14.8	82.2	540	5	BP065899	BP065899	C 756	14.8	82.2	631	6	CA583222	Wlms96.pko
684	14.8	82.2	541	8	A2853263	2M015820	C 757	14.8	82.2	631	7	CK980367	4112070.B
685	14.8	82.2	541	9	CG637725	OST365317	C 758	14.8	82.2	634	7	CK980970	4112955.B
686	14.8	82.2	542	5	B0369011	B0369011	C 759	14.8	82.2	635	8	BB472878	BB472878
687	14.8	82.2	542	8	A2164305	SP_0075.B	C 760	14.8	82.2	635	8	BH005272	BH005272
688	14.8	82.2	542	9	CG661037	OST441628	C 761	14.8	82.2	636	1	AJ638168	AJ638168
689	14.8	82.2	544	1	AA261070	mz81902.r	C 762	14.8	82.2	636	5	BU345482	603524630
690	14.8	82.2	546	7	CK437126	GO0044.BR	C 763	14.8	82.2	636	9	CE639866	tigr-gss-
691	14.8	82.2	546	9	CG661032	OST441621	C 764	14.8	82.2	637	4	BI267889	NFI11G84I
692	14.8	82.2	547	8	AA143192	SP_0028.B	C 765	14.8	82.2	637	4	BY717122	BY717122
693	14.8	82.2	547	9	CG667023	OST458877	C 766	14.8	82.2	638	6	CA648293	wrein.pko
694	14.8	82.2	547	9	CG670179	OST469027	C 767	14.8	82.2	638	6	BH043566	RPCI-24-3
695	14.8	82.2	548	4	BI443344	dal189h12.	C 768	14.8	82.2	639	7	CN918578	030205ABP
696	14.8	82.2	548	5	BU992790	BD11K08.r	C 769	14.8	82.2	642	6	CB576402	CB576402
697	14.8	82.2	548	9	CG667511	OST461205	C 770	14.8	82.2	643	7	CK438780	GO0031A.T
698	14.8	82.2	553	9	CG637709	OST365282	C 771	14.8	82.2	647	5	BP109223	BP109223
699	14.8	82.2	555	4	BI168630	RE09450.S	C 772	14.8	82.2	648	8	BH514367	BOGP238TF
700	14.8	82.2	555	4	BI168630	RE09450.S	C 773	14.8	82.2	648	9	CR057925	Forward.B
701	14.8	82.2	556	9	CG113183	PUIKQ17TD	C 774	14.8	82.2	651	6	CA123794	SCMCLR112
702	14.8	82.2	557	8	BH616017	BMEAC305H	C 775	14.8	82.2	651	6	BH762615	BH762615
703	14.8	82.2	560	6	CD878351	AZ04.1021	C 776	14.8	82.2	652	5	BU487978	604124894
704	14.8	82.2	560	8	AQ387146	RPCI11-15	C 777	14.8	82.2	653	2	BA442503	BA442503
705	14.8	82.2	561	7	CF634974	zmrw000.0	C 778	14.8	82.2	653	5	BU028629	QHR2A06.Y
706	14.8	82.2	563	4	BM180600	GAJ37604.	C 779	14.8	82.2	653	5	BU028629	QHR2A06.Y
707	14.8	82.2	563	7	CK444344	GO0071.TB	C 780	14.8	82.2	653	6	BY758054	BY758054
708	14.8	82.2	566	9	CE562828	tigr-gss-	C 781	14.8	82.2	653	9	AG081581	Pan.trog1
709	14.8	82.2	566	6	CD490869	WHE3007.C	C 782	14.8	82.2	654	8	A2966749	A2966749
710	14.8	82.2	567	9	CG638047	OST366684	C 783	14.8	82.2	656	5	BQ211295	UI-R-DY1-
711	14.8	82.2	571	4	BI448729	dag68b1.0	C 784	14.8	82.2	657	8	AQ048529	CLM-8C10-
712	14.8	82.2	571	8	AQ247764	Sheared.D	C 785	14.8	82.2	661	6	CA060053	SSA19B50
713	14.8	82.2	572	8	A2728421	RPCI-24-1	C 786	14.8	82.2	662	1	AV255774	AV255774
714	14.8	82.2	575	1	AA276208	vc40e08.r	C 787	14.8	82.2	662	2	BE492625	WHE0561.G
715	14.8	82.2	577	6	CF215482	CAST0002	C 788	14.8	82.2	663	1	AL885546	AL885546
716	14.8	82.2	578	7	CK423278	CK423278	C 789	14.8	82.2	666	9	CR324875	Medicago
717	14.8	82.2	579	4	BI379006	BFLG1.000	C 790	14.8	82.2	666	9	CG187574	PUMFM69TB
718	14.8	82.2	581	8	A2449569	LM0247D20	C 791	14.8	82.2	666	9	CG187575	PUMFM69TD
719	14.8	82.2	582	1	AJ638167	AJ638167	C 792	14.8	82.2	669	2	B5261440	B5261440
720	14.8	82.2	583	2	BF040254	BF250013B	C 793	14.8	82.2	669	5	BX4845287	BX4845287
721	14.8	82.2	585	1	AA673142	vc40f04.r	C 794	14.8	82.2	671	5	BU352287	603526612
722	14.8	82.2	585	8	BS7061	CIT-HSP-200	C 795	14.8	82.2	671	8	BZ097507	CH230-216
723	14.8	82.2	587	6	CF215707	CAST0002	C 796	14.8	82.2	672	5	BU300830	603732596
724	14.8	82.2	587	7	CF403148	CSECS001E	C 797	14.8	82.2	673	8	BH675273	BOMAD70TR
725	14.8	82.2	588	9	CF484490	Medicago	C 798	14.8	82.2	674	5	BU267067	603815073
726	14.8	82.2	593	2	BE973350	Medicago	C 799	14.8	82.2	677	8	BH967580	odg74e12.
727	14.8	82.2	593	7	CO204849	WS0062.B2	C 800	14.8	82.2	677	9	CG441176	CG441176
728	14.8	82.2	594	7	CK370829	zmrw0005	C 801	14.8	82.2	678	5	BU271554	603374448
729	14.8	82.2	596	9	CG588698	OST239930	C 802	14.8	82.2	678	5	BU271554	603374448
730	14.8	82.2	599	6	CA218993	SCJFAD1C1	C 803	14.8	82.2	679	9	AG133064	603144661
731	14.8	82.2	599	6	CA655917	wlmo.pko0	C 804	14.8	82.2	679	9	AG133064	Pan.trog1
732	14.8	82.2	600	5	BU921386	6083-60.M	C 805	14.8	82.2	680	5	BU463177	603366623
733	14.8	82.2	600	6	CB297280	12B22035	C 806	14.8	82.2	680	8	A2998500	2M0285B06
734	14.8	82.2	602	2	BF491201	AT27888.5	C 807	14.8	82.2	680	8	B58994	CIT-HSP-202
735	14.8	82.2	602	5	BU373780	603513477	C 808	14.8	82.2	681	2	BB199290	BB199290
736	14.8	82.2	605	6	BU921115	VVD050C04	C 809	14.8	82.2	683	2	BB199290	BB199290
737	14.8	82.2	605	8	BH764799	BMBAC351H	C 810	14.8	82.2	683	4	AG179784	603343562
738	14.8	82.2	606	2	BE534632	601233574	C 811	14.8	82.2	683	9	AG179784	Pan.trog1
739	14.8	82.2	606	9	CE601485	tigr-gss-	C 812	14.8	82.2	684	4	BH679653	UI-E-S00-
740	14.8	82.2	608	6	CA297318	SCUTS2208	C 813	14.8	82.2	684	6	CD715110	VWR208C09
741	14.8	82.2	608	7	CN850629	000928AAF	C 814	14.8	82.2	684	7	CO238124	WS0074.B2
742	14.8	82.2	609	7	CN910815	030221ABL	C 815	14.8	82.2	684	8	B2016630	oe157606.
743	14.8	82.2	612	7	CK533658	rsweb0.00	C 816	14.8	82.2	686	7	CK41151	030124ABL
744	14.8	82.2	616	2	AW741845	ug99e02.x	C 817	14.8	82.2	687	7	CN910143	030124ABL
745	14.8	82.2	617	9	CG684245	OGUKO87TH	C 818	14.8	82.2	687	7	CN910143	030124ABL
746	14.8	82.2	618	4	BJ067584	BJ067584	C 819	14.8	82.2	689	7	AQ552287	Sheared.D
747	14.8	82.2	618	8	BH768407	BMEAC377G	C 820	14.8	82.2	690	7	CK443998	Q00013A.T
748	14.8	82.2	618	9	CE096835	tigr-gss-	C 821	14.8	82.2	691	1	AA528354	nebs04.s
749	14.8	82.2	619	2	BF640958	NF039D121	C 822	14.8	82.2	692	7	CK436829	Q00044.TB
750	14.8	82.2	619	6	CB922358	VVD082G01	C 823	14.8	82.2	692	8	BH974819	BF974819
751	14.8	82.2	620	2	AW641181	cm04c05.w	C 824	14.8	82.2	693	5	CE334515	tigr-gss-
752	14.8	82.2	622	7	CF438748	EST675093	C 825	14.8	82.2	694	5	BU398123	603533895
753	14.8	82.2	625	7	CN815592	HFO4513.D	C 826	14.8	82.2	697	2	BF486559	AT20888.5
754	14.8	82.2	628	5	BU117338	603140205	C 827	14.8	82.2	697	9	CU587194	OB_BA008



C 828	14.8	82.2	698	5	BU399096	603536496	BU399096	603536496	C 901	14.8	82.2	749	8	BZ819969	BZ819969	PUEU01TD
C 829	14.8	82.2	698	5	BU399169	603534935	BU399169	603534935	902	14.8	82.2	753	4	BG972101	BG972101	602838623
C 830	14.8	82.2	698	7	CO477525	CO477525	CO477525	CO477525	903	14.8	82.2	753	4	CO020005	CO020005	PUEB034TD
C 831	14.8	82.2	699	5	BU281038	603599632	BU281038	603599632	904	14.8	82.2	756	5	BH359995	BH359995	CH230-126
C 832	14.8	82.2	699	5	BU399454	603534217	BU399454	603534217	905	14.8	82.2	757	5	BU354750	BU354750	CH230-126
C 833	14.8	82.2	699	8	BH585199	BOGRP42TF	BH585199	BOGRP42TF	C 906	14.8	82.2	760	9	CR629664	CR629664	CH240-303
C 834	14.8	82.2	699	5	CE182515	tigr-gss-	CE182515	tigr-gss-	C 907	14.8	82.2	761	7	CR629664	CR629664	DKF2p4690
C 835	14.8	82.2	701	5	BU339406	603513054	BU339406	603513054	908	14.8	82.2	763	5	BU365883	BU365883	60355685
C 836	14.8	82.2	702	4	BG333308	602431343	BG333308	602431343	C 909	14.8	82.2	763	9	AG564394	AG564394	Mus muscu
C 837	14.8	82.2	703	2	AW940990	GH2431343	AW940990	GH2431343	C 910	14.8	82.2	764	5	BU359263	BU359263	603478572
C 838	14.8	82.2	703	7	CO233862	WS0058.B2	CO233862	WS0058.B2	C 911	14.8	82.2	764	7	CK311084	CK311084	SB0203682
C 839	14.8	82.2	704	6	CAB15165	CA2EI202	CAB15165	CA2EI202	912	14.8	82.2	765	5	BU255581	BU255581	603742821
C 840	14.8	82.2	705	9	AG106618	Pan trogl	AG106618	Pan trogl	913	14.8	82.2	765	6	CD356060	CD356060	AGENCOURT
C 841	14.8	82.2	706	9	AG479198	Mus muscu	AG479198	Mus muscu	914	14.8	82.2	767	8	AZ840499	AZ840499	2M0138006
C 842	14.8	82.2	707	5	BU393020	603857648	BU393020	603857648	915	14.8	82.2	768	9	AG515925	AG515925	Mus muscu
C 843	14.8	82.2	707	6	CD763316	GGEZEM100	CD763316	GGEZEM100	916	14.8	82.2	768	9	AV404219	AV404219	Mus muscu
C 844	14.8	82.2	707	7	CO489261	CO02510.B	CO489261	CO02510.B	917	14.8	82.2	768	9	CC925421	CC925421	t083117ba
C 845	14.8	82.2	707	7	CO489514	GH02510.B	CO489514	GH02510.B	918	14.8	82.2	769	4	BH983111	BH983111	602305819
C 846	14.8	82.2	708	5	BU231540	603401224	BU231540	603401224	919	14.8	82.2	771	5	BU244342	BU244342	603780868
C 847	14.8	82.2	711	1	AI405652	GH25733.5	AI405652	GH25733.5	920	14.8	82.2	775	9	BX985468	BX985468	Reverse s
C 848	14.8	82.2	711	7	CO488308	GH02511.B	CO488308	GH02511.B	C 921	14.8	82.2	776	8	CC443091	CC443091	PUEUHY38TD
C 849	14.8	82.2	712	7	CO489543	GH02510.B	CO489543	GH02510.B	922	14.8	82.2	778	6	CA323361	CA323361	UI-M-FX0-
C 850	14.8	82.2	713	5	BU708787	UI-M-FIO	BU708787	UI-M-FIO	923	14.8	82.2	780	4	B1517407	B1517407	603041665
C 851	14.8	82.2	713	6	CB339948	CA23RI021	CB339948	CA23RI021	C 924	14.8	82.2	780	7	CR819415	CR819415	EST696797
C 852	14.8	82.2	714	4	BG016479	GF73A04.X	BG016479	GF73A04.X	C 925	14.8	82.2	784	5	BU471530	BU471530	603364968
C 853	14.8	82.2	714	8	BZ088637	11a57a03.	BZ088637	11a57a03.	C 926	14.8	82.2	785	9	CL729733	CL729733	OR_EBA006
C 854	14.8	82.2	714	9	CE111603	tigr-gss-	CE111603	tigr-gss-	C 927	14.8	82.2	786	5	BU383324	BU383324	603583349
C 855	14.8	82.2	714	9	AG287524	Mus muscu	AG287524	Mus muscu	C 928	14.8	82.2	787	7	CO032955	CO032955	EST811339
C 856	14.8	82.2	716	6	CB339858	CA23RI021	CB339858	CA23RI021	C 929	14.8	82.2	787	9	CC562635	CC562635	CH240.473
C 857	14.8	82.2	716	7	CK429222	GQ0013b.T	CK429222	GQ0013b.T	C 930	14.8	82.2	788	8	AZ197715	AZ197715	SP.1035.B
C 858	14.8	82.2	717	8	AZ562609	RFCI-23-1	AZ562609	RFCI-23-1	931	14.8	82.2	788	8	AG601361	AG601361	Mus muscu
C 859	14.8	82.2	717	7	CF816398	EST693780	CF816398	EST693780	932	14.8	82.2	788	9	CC558791	CC558791	CH240.467
C 860	14.8	82.2	717	9	CG441168	AGVHPD68TH	CG441168	AGVHPD68TH	C 933	14.8	82.2	789	9	CO017898	CO017898	EST788280
C 861	14.8	82.2	720	7	CO033121	EST811505	CO033121	EST811505	C 934	14.8	82.2	789	6	CD849704	CD849704	DH0AC0232
C 862	14.8	82.2	720	9	AG410410	Mus muscu	AG410410	Mus muscu	C 935	14.8	82.2	790	6	CD849704	CD849704	DH0AC0232
C 863	14.8	82.2	721	7	CK683692	ZF101-P00	CK683692	ZF101-P00	C 936	14.8	82.2	792	8	AQ163247	AQ163247	mgx00023F
C 864	14.8	82.2	722	5	BU382168	603856807	BU382168	603856807	C 937	14.8	82.2	793	7	CF518980	CF518980	CAP0006.I
C 865	14.8	82.2	722	6	CD763336	GGEZEM100	CD763336	GGEZEM100	C 938	14.8	82.2	793	7	CO024073	CO024073	EST789206
C 866	14.8	82.2	723	5	BU285659	603862416	BU285659	603862416	C 939	14.8	82.2	794	5	BU2664754	BU2664754	603814859
C 867	14.8	82.2	728	5	BU214711	603759266	BU214711	603759266	C 940	14.8	82.2	796	5	BP737339	BP737339	BP737339
C 868	14.8	82.2	728	6	CAL160938	SCWCR2306	CAL160938	SCWCR2306	C 941	14.8	82.2	796	5	BU383365	BU383365	603581454
C 869	14.8	82.2	728	8	BH983477	MB61p6D2b	BH983477	MB61p6D2b	C 942	14.8	82.2	797	6	CA270993	CA270993	SCRULB206
C 870	14.8	82.2	728	9	CR294477	Medicago	CR294477	Medicago	C 943	14.8	82.2	797	9	CR214672	CR214672	Reverse s
C 871	14.8	82.2	729	9	CO210082	WS00817.B	CO210082	WS00817.B	944	14.8	82.2	798	5	BX884930	BX884930	603586677
C 872	14.8	82.2	729	8	AZ059830	RFCI-23-4	AZ059830	RFCI-23-4	C 945	14.8	82.2	799	9	BU367150	BU367150	603586667
C 873	14.8	82.2	730	7	CO244168	WS0037.B2	CO244168	WS0037.B2	C 946	14.8	82.2	800	5	BU368506	BU368506	603586667
C 874	14.8	82.2	731	1	AJ615476	AJ615476	AJ615476	AJ615476	947	14.8	82.2	801	5	CO017843	CO017843	AGENCOURT
C 875	14.8	82.2	731	8	BH939285	odg56a10.	BH939285	odg56a10.	C 948	14.8	82.2	801	7	CO559295	CO559295	AGENCOURT
C 876	14.8	82.2	732	5	BU364102	603789260	BU364102	603789260	C 949	14.8	82.2	802	7	BU448902	BU448902	603765928
C 877	14.8	82.2	733	5	BU270012	603509414	BU270012	603509414	C 950	14.8	82.2	804	7	CK476384	CK476384	AGENCOURT
C 878	14.8	82.2	733	9	AG179972	Pan trogl	AG179972	Pan trogl	C 951	14.8	82.2	806	5	BU570064	BU570064	AGENCOURT
C 879	14.8	82.2	734	5	BU140394	603137507	BU140394	603137507	C 952	14.8	82.2	807	5	BU285524	BU285524	603501289
C 880	14.8	82.2	735	5	BU270002	603818131	BU270002	603818131	C 953	14.8	82.2	807	5	CF212598	CF212598	CGF100065
C 881	14.8	82.2	735	9	AG374946	Mus muscu	AG374946	Mus muscu	954	14.8	82.2	814	5	BU255201	BU255201	603747083
C 882	14.8	82.2	737	6	CP232861	PtaJX0001	CP232861	PtaJX0001	C 955	14.8	82.2	814	7	CF515257	CF515257	CAP0001.I
C 883	14.8	82.2	737	9	CG917925	HSC.01003	CG917925	HSC.01003	C 956	14.8	82.2	815	5	BU143087	BU143087	603137945
C 884	14.8	82.2	740	8	AQ558602	RFCI-11-3	AQ558602	RFCI-11-3	C 957	14.8	82.2	817	7	CF783693	CF783693	AGENCOURT
C 885	14.8	82.2	741	5	BU338438	603513344	BU338438	603513344	958	14.8	82.2	817	7	CR421806	CR421806	CR421806
C 886	14.8	82.2	741	7	CO397113	AGENCOURT	CO397113	AGENCOURT	959	14.8	82.2	820	2	BF617635	BF617635	HVSNEC001
C 887	14.8	82.2	741	7	CR550222	DKF2P459N	CR550222	DKF2P459N	C 960	14.8	82.2	820	2	BF617635	BF617635	HVSNEC001
C 888	14.8	82.2	742	5	BU295077	603577613	BU295077	603577613	C 961	14.8	82.2	822	7	CK773189	CK773189	961600.MA
C 889	14.8	82.2	742	7	CO064641	est.k.bre	CO064641	est.k.bre	962	14.8	82.2	822	8	BZ785297	BZ785297	FUGFA87TB
C 890	14.8	82.2	742	9	BX155786	Danio rer	BX155786	Danio rer	C 963	14.8	82.2	822	9	CL011217	CL011217	ZMMBBB053
C 891	14.8	82.2	743	6	CB975130	CAB30006	CB975130	CAB30006	964	14.8	82.2	824	9	CC747854	CC747854	ZMMBBB053
C 892	14.8	82.2	743	7	CO252938	WS00818.B	CO252938	WS00818.B	965	14.8	82.2	825	5	BU366695	BU366695	603586571
C 893	14.8	82.2	743	7	CO253075	WS00818.B	CO253075	WS00818.B	C 966	14.8	82.2	828	7	CF516346	CF516346	CAP0003.I
C 894	14.8	82.2	743	7	CO571303	AGENCOURT	CO571303	AGENCOURT	967	14.8	82.2	828	7	CF516346	CF516346	CAP0003.I
C 895	14.8	82.2	743	8	BZ373303	ie77908.b	BZ373303	ie77908.b	C 968	14.8	82.2	833	6	CA815191	CA815191	CA12EI202
C 896	14.8	82.2	744	5	BU269413	603817429	BU269413	603817429	C 969	14.8	82.2	833	7	CF345911	CF345911	AGENCOURT
C 897	14.8	82.2	745	2	BF139363	601785226	BF139363	601785226	C 970	14.8	82.2	834	5	BU323127	BU323127	603490006
C 898	14.8	82.2	745	5	BX736669	601785226	BX736669	601785226	C 971	14.8	82.2	836	8	CC420276	CC420276	FUHKM56TD
C 899	14.8	82.2	747	5	BU307316	603740142	BU307316	603740142	C 972	14.8	82.2	838	5	BU384509	BU384509	603861447
C 900	14.8	82.2	749	7	CK95											

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974 14.8 82.2 844 9 AG329955 Mus muscu
c 975 14.8 82.2 846 5 BU114544
c 976 14.8 82.2 851 6 CA817210
c 977 14.8 82.2 855 5 BU440218
c 978 14.8 82.2 858 7 CO365914
c 979 14.8 82.2 859 5 BU261147
c 980 14.8 82.2 859 6 CA817151
c 981 14.8 82.2 862 5 BU293725
c 982 14.8 82.2 864 7 CO234999
c 983 14.8 82.2 865 8 CO378163
c 984 14.8 82.2 869 6 CO232652
c 985 14.8 82.2 869 7 CF822131
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c 987 14.8 82.2 870 6 CB574907
c 988 14.8 82.2 871 5 BU326362
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## ALIGNMENTS

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RESULT 1
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DEFINITION lM016G09F Mouse 10kb plasmid UGCM library Mus musculus genomic
clone UGCM1016G09 F, genomic survey sequence.
ACCESSION AZ400033
VERSION AZ400033.1 GI:10515107
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 319)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A., and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0166 row: G column: 09
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 319.
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/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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## ORIGIN

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Query Match 91.1%; Score 16.4; DB 8; Length 319;
Best Local Similarity 94.4%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ATGCTGGTACTGGCTG 18
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DB 195 ATGCTGATCTGGCTG 178
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## RESULT 2

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LOCUS CE120751/c 335 bp DNA linear GSS 25-SEP-2003
DEFINITION tigr-gss-dog-17000325906132 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE120751
VERSION CE120751.1 GI:35216152
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 335)
Kirkness, E.F., Baina, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-538-0200
Fax: 301-538-0208
Email: ekirknes@tigr.org
Class: shotgun.
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/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

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## FEATURES

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Location/Qualifiers
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peripheral blood"

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## ORIGIN

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Query Match 91.1%; Score 16.4; DB 9; Length 335;
Best Local Similarity 94.4%; Pred. No. 1.1e+03;

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Matches	17;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
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Db	333	ATGCTAGGTACTTGGCTG	316						
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ACCESSION	AI181139								
VERSION	AI181139.1								
KEYWORDS	EST.								
SOURCE	Mus musculus (house mouse)								
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 380)								
REFERENCE	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.								
AUTHORS	The WashU-HMI Mouse EST Project								
TITLE	Unpublished (1996)								
JOURNAL	Contact: Marra M/Mouse EST Project								
COMMENT	WashU-HMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:907956 Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 346.								
FEATURES	Location/Qualifiers								
source	1. 380 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="IMAGE:1396240" /sex="male" /tissue_type="mammary gland" /dev_stage="4 weeks" /lab_host="DH10B" /clone_lib="Soares mammary gland NbMMG" /note="Organ: mammary gland; Vector: pTV73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAGTGGCGGCGCGAATGGTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTV73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."								
ORIGIN									
Query Match	91.1%;	Score 16.4;	DB 1;	Length 380;					
Best Local Similarity	94.4%;	Pred. No. 1.1e+03;							
Matches	17;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	ATGCTTGGTACTTGGCTG	18						
Db	251	ATGCTTGTACTTGGCTG	234						
RESULT 4									
LOCUS	AI037754/c								
DEFINITION	ub51c05.r1 Soares mammary_gland NbMMG Mus musculus cDNA clone IMAGE:1381256 5', similar to gb:M94654 INTERLEUKIN ENHANCER-BINDING FACTOR (HUMAN) ;, mRNA sequence.								
ACCESSION	AI037754								
VERSION	AI037754.1								
KEYWORDS	EST.								
SOURCE	Mus musculus (house mouse)								
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 408)								
REFERENCE	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.								
AUTHORS	The WashU-HMI Mouse EST Project								
TITLE	Unpublished (1996)								
JOURNAL	Contact: Marra M/Mouse EST Project								
COMMENT	WashU-HMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:903724 Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 399.								
FEATURES	Location/Qualifiers								
source	1. 408 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="IMAGE:1381256" /sex="male" /tissue_type="mammary gland" /dev_stage="4 weeks" /lab_host="DH10B" /clone_lib="Soares mammary gland NbMMG" /note="Organ: mammary gland; Vector: pTV73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAGTGGCGGCGCGAATGGTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTV73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."								
ORIGIN									
Query Match	91.1%;	Score 16							

```

VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

B1110479.1 GI:14561380
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 408)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM11074 row: p column: 13
High quality sequence stop: 406.
Location/Qualifiers
1..408
/organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5026428"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam5"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

ORIGIN
Query Match 91.1%; Score 16.4; DB 4; Length 408;
Best Local Similarity 94.4%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTGGCTG 18
||||| |||||||
Db 61 ATGCTTGATCTGGCTG 44

RESULT 6
AA510488/c
LOCUS
DEFINITION
vhs4a10.r1 Soares mammary_gland NbMMG Mus musculus cDNA clone
IMAGE:890778 5' similar to gb:M94654 INTERLEUKIN ENHANCER-BINDING
FACTOR (HUMAN); mRNA sequence.
AA510488
AA510488.1 GI:2248342
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 424)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

FEATURES
source
1..424
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:890778"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares mammary gland NbMMG"
/notes="Organ: mammary gland; Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo (dt) primer [5',
TGTTCACATCTGAGTGGACGCGCGGATGCTTTTCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M. Fatima
Bonaldo."

ORIGIN
Query Match 91.1%; Score 16.4; DB 1; Length 424;
Best Local Similarity 94.4%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTGGCTG 18
||||| |||||||
Db 395 ATGCTTGATCTGGCTG 378

RESULT 7
CK332748/c
LOCUS
DEFINITION
H8213B02-5 NIA Mouse Unique Gene Set Version 2 Mus musculus CDNA
clone H8213B02 5', mRNA sequence.
CK332748
CK332748.1 GI:40232341
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 459)
VanBuren,V., Piao,Y., Dudekula,D.B., Qian,Y., Carter,M.G.,
Martin,P.R., Stagg,C.A., Basse,J., Aiba,K., Hamatani,T.,
Kargul,G.J., Luo,A.G., Kelso,J., Hide,W. and Ko,M.S.H.
Assembly, verification, and initial annotation of NIA 7.4K mouse
CDNA clone set
Genome Res. 12 (12), 1999-2003 (2002)
12466305
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@gsun.grc.nia.nih.gov
Plate: H8213 row: B column: 02
Seq primer: M13 Reverse
High quality sequence stop: 459
POLYA=No.
Location/Qualifiers

FEATURES

```

Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mousees@watson.wustl.edu  
This clone is available royalty-free through LML; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:518738

Seq primer: -28ml3 rev2 ET from Amersham  
High quality sequence stop: 407.

FEATURES  
source

1..424  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:890778"  
/sex="male"  
/tissue\_type="mammary gland"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"  
/clone\_lib="Soares mammary gland NbMMG"  
/notes="Organ: mammary gland; Vector: pT7T3D-Pac  
(Pharmacia) with a modified polylinker; Site 1: Not I;  
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -  
oligo (dt) primer [5',  
TGTTCACATCTGAGTGGACGCGCGGATGCTTTTCTTTTCTTTTCTTTTCTTTT  
T 3']; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT7T3 vector.  
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library  
constructed and normalized by Bento Soares and M. Fatima  
Bonaldo."

#### ORIGIN

Query Match 91.1%; Score 16.4; DB 1; Length 424;  
Best Local Similarity 94.4%; Pred. No. 1.2e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTGGCTG 18

||||| |||||||  
Db 395 ATGCTTGATCTGGCTG 378

#### RESULT 7

CK332748/c

LOCUS

DEFINITION

H8213B02-5 NIA Mouse Unique Gene Set Version 2 Mus musculus CDNA

clone H8213B02 5', mRNA sequence.

CK332748

CK332748.1 GI:40232341

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 459)

VanBuren,V., Piao,Y., Dudekula,D.B., Qian,Y., Carter,M.G.,

Martin,P.R., Stagg,C.A., Basse,J., Aiba,K., Hamatani,T.,

Kargul,G.J., Luo,A.G., Kelso,J., Hide,W. and Ko,M.S.H.

Assembly, verification, and initial annotation of NIA 7.4K mouse

CDNA clone set

Genome Res. 12 (12), 1999-2003 (2002)

12466305

Contact: Dawood B. Dudekula

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cdna@gsun.grc.nia.nih.gov

Plate: H8213 row: B column: 02

Seq primer: M13 Reverse

High quality sequence stop: 459

POLYA=No.

Location/Qualifiers

```

source
1. 459
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="niaEST:H8213B02-5"
/db_xref="taxon:10090"
/clone="H8213B02"
/sex="mixed"
/dev_stage="mixed"
/lab_host="DH10B"
/clone_lib="NIA Mouse Unique Gene Set Version 2"
/Note=Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This
clone is among a rearrayed set of 11,424 clones from more
than 20 cDNA libraries."

ORIGIN
Query Match 91.1%; Score 16.4; DB 7; Length 459;
Best Local Similarity 94.4%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGCTACTGGCTG 18
||||| |||||||
Db 245 ATGCTTGATACTGGCTG 228

RESULT 8
CA534216/c
LOCUS
DEFINITION CA534216-5N NIA Mouse 7.5-dpc Whole Embryo cDNA Library (Long) Mus
musculus cDNA clone NIA:CA0202E10 IMAGE:30010809 5', mRNA sequence.
ACCESSION CA534216.1 GI:25066199
VERSION EST.
KEYWORDS Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 503)
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Tanaka, T., Lim, M.K.,
Luo, A. and Ko, M.S.H.
Systematic Analyses of NIA Mouse 7.5-dpc Whole Embryo cDNA Library
(Long)
JOURNAL Unpublished (2001)
COMMENT Other ESTs: CA0202E10-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: CA0202 row: E column: 10
Seq primer: M13 Reverse
High quality sequence stop: 503
POLYA=No.

FEATURES
Location/Qualifiers
1..503
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="niaEST:H8213B02-5N"
/db_xref="taxon:10090"
/clone="NIA:CA0202E10 IMAGE:30010809"
/tissue_type="whole embryo including extraembryonic
tissues at 7.5-days postcoitum"
/dev_stage="7.5-days postcoitum"
/lab_host="DH10B"
/clone_lib="NIA Mouse 7.5-dpc Whole Embryo cDNA Library
(Long)"
/Note=Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This
clone is among a rearrayed set of 11,424 clones from more
than 20 cDNA libraries."

source
1. 459
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="niaEST:H8213B02-5"
/db_xref="taxon:10090"
/clone="H8213B02"
/sex="mixed"
/dev_stage="mixed"
/lab_host="DH10B"
/clone_lib="NIA Mouse Unique Gene Set Version 2"
/Note=Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This
clone is among a rearrayed set of 11,424 clones from more
than 20 cDNA libraries."

ORIGIN
Query Match 91.1%; Score 16.4; DB 6; Length 503;
Best Local Similarity 94.4%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGCTACTGGCTG 18
||||| |||||||
Db 283 ATGCTTGATACTGGCTG 266

RESULT 9
BE371450/c
LOCUS
DEFINITION BE371450-1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3591877 5',
mRNA sequence.
ACCESSION BE371450.1 GI:9316813
VERSION EST.
KEYWORDS Mus musculus (house mouse)
SOURCE
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 506)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8762 row: C column: 14
High quality sequence stop: 504.

FEATURES
Location/Qualifiers
1..506
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:3591877"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu29"
/Note=Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally; Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

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VERSION      BM511260.1  GI:18692403
KEYWORDS     EST.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE    1 (bases 1 to 583)
AUTHORS      Melton, D., Brown, J., Keny, G., Permutt, A., Lee, C., Kaestner, K.,
              Hillier, L., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
              Haller, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
              Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
              Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R.,
              Williams, T., Jackson, Y., and Bowers, Y.
              Endocrine Pancreas Consortium
              Unpublished (2000)
              Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
              Endocrine Pancreas Consortium
              Harvard University, Howard Hughes Medical Institute
              Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
              MA 02138
              Tel: 617-495-1812
              Fax: 617-495-8557
              Email: dmelton@bioph.harvard.edu
              Library was constructed by Dr. Douglas Melton DNA sequencing by:
              Washington University Genome Sequencing Center For information on
              obtaining a clone please contact: Juliana Brown
              (brown@fas.harvard.edu)
              MGI:1956888 This sequence now available from the IMAGE consortium,
              for clone orders contact: info@image.llnl.gov
              Seq primer: -40RP from Gibco
              High quality sequence stop: 432.
              Location/Qualifiers
                source
                  1..583
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                  /mol_type="mRNA"
                  /strain="ICR"
                  /db_xref="taxon:10090"
                  /clone="IMAGE:5679010"
                  /sex="Both"
                  /tissue_type="Total pancreas"
                  /dev_stage="Embryonic day 16.5"
                  /lab_host="TOP10"
                  /clone_lib="Melton Mouse E16 5 Pancreas Library 2 M16B2"
                  /note="Organ: Pancreas; Vector: pBluescript II SK; Site_1:
                  NotI; Site 2: SalI; Library constructed using Superscript
                  Plasmid Library kit (Life Technologies). cDNA made by
                  oligo-dT priming. Size-selected by column fractionation;
                  average insert size 1.06kb. Primary library,
                  unamplified."

ORIGIN
  Query Match      91.1%; Score 16.4; DB 4; Length 583;
  Best Local Similarity 94.4%; Pred. No. 1.2e+03;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGACTTGCTG 18
    ||||| ||||| |||||
Db 204 ATGCTGATGACTTGCTG 187

RESULT 13
LOCUS      BQ339445          584 bp  mRNA  linear  EST 20-MAY-2002
DEFINITION MR3-NN0216-031100-007-d07 NN0216 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BQ339445
VERSION    BQ339445.1  GI:20999109
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 584)
REFERENCE  Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

VERSION      BZ185412      584 bp  DNA  linear  GSS 11-OCT-2002
KEYWORDS     CH230-340N3.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
SOURCE       CH230-340N3, genomic survey sequence.
ACCESSION    BZ185412
VERSION      BZ185412.1  GI:23836023
KEYWORDS     GSS.
SOURCE       Rattus norvegicus (Norway rat)
ORGANISM     Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
            1 (bases 1 to 584)
REFERENCE    Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
            Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
            Riggs, F., de Jong, P., and Fraser, C.M.
            Rat BAC End Sequences from Library CHORI-230 MboI segment
            Unpublished (1999)
            Other GSSs: CH230-340N3.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA

```

```

TITLE       Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P.,
              Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
              Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
              O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
              Simpson, A.J.
              Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
              Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
              20202663
              10737800
              PUBLISHED
              COMMENT
              Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?l1=MR3t2-MR3-NN0216-
              031100-007-d07&t3=2000-11-03&t4=1)
              Seq primer: puc 18 forward
              High quality sequence stop: 7.
              Location/Qualifiers
                source
                  1..584
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /dev_stage="Adult"
                  /clone_lib="NN0216"
                  /note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
                  Site_2: SmaI; A mini-library was made by cloning products
                  derived from ORESTES PCR (U.S. Letters Patent application
                  No. 196,716 - Ludwig Institute for Cancer Research)
                  profiles into the pUC 18 vector. Reverse transcription of
                  tissue mRNA and cDNA amplification were performed under
                  low stringency conditions."

ORIGIN
  Query Match      91.1%; Score 16.4; DB 5; Length 584;
  Best Local Similarity 94.4%; Pred. No. 1.2e+03;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGACTTGCTG 18
    ||||| ||||| |||||
Db 109 ATGCTTGACTTGATG 126

RESULT 14
BZ185412/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230  
(<http://www.chori.org/bacpac/rat230.htm>). For BAC library  
availability, please contact Pieter de Jong ([pdejong@mail.choi.org](mailto:pdejong@mail.choi.org)).  
Clones may be purchased from BACPAC Resources  
([http://www.chori.org/bacpac/orering\\_information.htm](http://www.chori.org/bacpac/orering_information.htm)). BAC end  
page: [http://www.tigr.org/tldb/bac\\_ends/rat/bac\\_end\\_intro.html](http://www.tigr.org/tldb/bac_ends/rat/bac_end_intro.html)  
Plate: 340 row: N column: 3  
Seq primer: SP6  
Class: BAC ends.

#### FEATURES

Location/Qualifiers  
1. 584  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/strain="BN/SHHed/MCW"  
/db\_xref="taxon:10116"  
/clone="CH230-340N3"  
/sex="female"  
/cell\_type="Brain"  
/clone\_lib="CHORI-230 Segment 2"  
/note="Vector: PTABRAC1.3; Site 1: WbOI; Site 2: MbOI;  
CHORI-230 Rat (BN/SHHed/MCW) BAC library produced by  
Pieter de Jong"

#### ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 584;  
Best Local Similarity 94.4%; Pred. No. 1.2e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGCTTGCTACTTGCTG 18  
|||||  
DB 504 ATGCTTGCTCTGCTG 487  
|||||

#### RESULT 15

BI986945/c  
LOCUS 3183-96 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA, EST 20-DEC-2001  
DEFINITION mRNA sequence.

ACCESSION BI986945

VERSION BI986945.1 GI:17957905

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

#### ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 600)  
Mu.X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W.,  
White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Klein, W.H.  
Gene expression in the developing mouse retina by EST sequencing  
and microarray analysis  
Nucleic Acids Res. 29 (24), 4983-4993 (2001)

#### JOURNAL

#### MEDLINE

#### PUBMED

#### COMMENT

Contact: Klein WH  
Department of Biochemistry and Molecular Biology  
University of Texas M.D. Anderson Cancer Center  
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA  
Tel: 713 792 3646  
Fax: 713 790 0329.

#### FEATURES

Location/Qualifiers  
1. 600  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/tissue\_type="neural retina"  
/dev\_stage="embryonic day 14.5 post-fertilization"  
/clone\_lib="Mouse E14.5 retina lambda ZAP II Library"

#### ORIGIN

Query Match 91.1%; Score 16.4; DB 4; Length 600;

Best Local Similarity 94.4%; Pred. No. 1.3e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTTGCTG 18

|||||

DB 119 ATGCTTGCTACTTGCTG 102

#### RESULT 16

#### BI987005/c

#### LOCUS

#### DEFINITION

BI987005 600 bp mRNA linear EST 20-DEC-2001

3184-66 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,

mRNA sequence.

ACCESSION BI987005

VERSION BI987005.1 GI:17957966

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 600)

AUTHORS Mu.X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W.,

White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Klein, W.H.

Gene expression in the developing mouse retina by EST sequencing

and microarray analysis

Nucleic Acids Res. 29 (24), 4983-4993 (2001)

JOURNAL 21671825

MEDLINE 11812828

PUBMED

COMMENT Contact: Klein WH

Department of Biochemistry and Molecular Biology

University of Texas M.D. Anderson Cancer Center

Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA

Tel: 713 792 3646

Fax: 713 790 0329.

Location/Qualifiers

1. 600

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/tissue\_type="neural retina"

/dev\_stage="embryonic day 14.5 post-fertilization"

/clone\_lib="Mouse E14.5 retina lambda ZAP II Library"

ORIGIN

Query Match 91.1%; Score 16.4; DB 4; Length 600;

Best Local Similarity 94.4%; Pred. No. 1.3e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTTGCTG 18

|||||

DB 119 ATGCTTGCTACTTGCTG 102

#### RESULT 17

#### BI987217/c

#### LOCUS

#### DEFINITION

BI987217 600 bp mRNA linear EST 20-DEC-2001

3193-11 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,

mRNA sequence.

ACCESSION BI987217

VERSION BI987217.1 GI:17958179

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 600)

AUTHORS Mu.X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W.,

White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Klein, W.H.

Gene expression in the developing mouse retina by EST sequencing

and microarray analysis

Nucleic Acids Res. 29 (24), 4983-4993 (2001)

JOURNAL 21671825

MEDLINE 11812828

PUBMED



```

Contact: Klein WH
Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.

FEATURES
    source
        Location/Qualifiers
            1..600
                /organism="Mus musculus"
                /mol_type="mRNA"
                /db_xref="taxon:10090"
                /tissue_type="neural retina"
                /dev_stage="embryonic day 14.5 post-fertilization"
                /clone_lib="Mouse E14.5 retina lambda ZAP II Library"

ORIGIN
Query Match          91.1%; Score 16.4; DB 4; Length 600;
Best Local Similarity 94.4%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  ATGCTTGCTACTTGGCTG 18
        |||||  |||||
DB      119  ATGCTTGATCTTGGCTG 102

RESULT 18
BF658039/c
LOCUS      BF658039                604 bp      mRNA      linear      EST 20-DEC-2000
DEFINITION ma94d01.Y1 Soares thymus 2NbMT Mus musculus cDNA clone
IMAGE:3824305 5', mRNA sequence.
ACCESSION BF658039
VERSION    BF658039.1  GI:11923173
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS    NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Other ESTs: ma94d01.x1
            Contact: Robert Strausberg, Ph.D.
            Email: cgapsb-remail.nih.gov
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1460657
            Seg primer: -40RP from Gibco
            High quality sequence stop: 413.

FEATURES
    source
        Location/Qualifiers
            1..604
                /organism="Mus musculus"
                /mol_type="mRNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="IMAGE:3824305"
                /sex="male"
                /tissue_type="Thymus"
                /dev_stage="4 weeks"
                /lab_host="DHI10B"
                /clone_lib="Soares thymus 2NbMT"
                /note="vector: p7T3b-Pac (Pharmacia) with a modified
                polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
                was primed with a Not I - oligo(dT) primer [5',
                TGTTCACCAATCTGAAGTGGGCGCGCTTTTATTTTATTTT
                3']; double-stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Not I and cloned into the Not I
                and Eco RI sites of the modified p7T3 vector. RNA
                provided by Dr. Bertrand Jordan. Library went through two
                rounds of normalization, and was constructed by Bento
                Soares and M.Fatima Bonaldo."

```



**AUTHORS** Bonaldo,M.F., Lennon,G. and Soares,M.B.  
**TITLE** Normalization and subtraction: two approaches to facilitate gene discovery  
**JOURNAL** Genome Res. 6 (9), 791-806 (1996)  
**MEDLINE** 97044477  
**PUBMED** 8889548  
**COMMENT** Contact: Chin, H  
National Institute of Mental Health  
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: mEST@mail.nih.gov  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Genetic Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com).  
Seq primer: M13 FORWARD  
POLYA=Yes.

**FEATURES**  
source

**FEATURES** Location/Qualifiers  
1..639  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clones="UI-M-AQO-cit-k-14-0-UI"  
/dev\_stage="27-32 days"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NIH BMAP MHI"  
/note="Vector: p773D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; The  
NIH BMAP MHI library is a non-normalized library  
constructed from mouse hippocampus. The tag is a string  
of 5 nucleotides present between the Not I site and the  
oligo-dT track. The library was constructed as described  
by Bonaldo, Lennon and Soares, Genome Research 6:  
791-806, 1996. Tissue provided by Ms. Annie Novakovich,  
Zivic-Miller Laboratories.  
TAG\_TISSUE=hippocampus  
TAG\_LIB=UI-M-AQO  
TAG\_SEQ=TTTCCA"

**ORIGIN**

Query Match 91.1%; Score 16.4; DB 6; Length 639;  
Best Local Similarity 94.4%; Pred. No. 1.3e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 ATGCTTGGTACTTGGCTG 18  
|||||  
Db 312 ATGCTTGATCTTGGCTG 295  
|||||

**RESULT 23**  
**BM206907** BM206907 574 bp mRNA linear EST 08-JUN-2003  
**LOCUS** C0605A09-3 NIA Mouse Trophoblast Stem Cell cDNA Library (long) Mus  
musculus cDNA clone NIA:C0605A09 IMAGE:30020648 3', mRNA sequence.  
**DEFINITION** BM206907  
**ACCESSION** BM206907  
**VERSION** BM206907.2 GI:31531041  
**KEYWORDS** EST.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 674)  
Piao,X., Ko,N.T., Lim,M.K. and Ko,M.S.H.  
**AUTHORS** Construction of long-transcript enriched cDNA libraries from  
submicrogram amounts of total RNAs by a universal PCR amplification  
method  
**TITLE** Genome Res. 11 (9), 1553-1558 (2001)  
**JOURNAL** 21429098  
**MEDLINE** 11544199  
**PUBMED**

**COMMENT**

On Dec 14, 2001 this sequence version replaced gi:17762571.  
Other\_ESTs: C0605A09-5N  
Contact: Dawood B. Dudekula  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6620, USA  
Email: cdna@gsun.grc.nia.nih.gov  
Plate: C0605 row: A column: 09  
Seq primer: 21M13 Forward  
High quality sequence stop: 674  
POLYA=Yes.

**FEATURES**  
Location/Qualifiers  
1..674

/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="B6/EGFP transgenic ICR mice"  
/db\_xref="niaEST:C0605A09-3"  
/db\_xref="taxon:10090"  
/clone="NIA:C0605A09 IMAGE:30020648"  
/tissue\_type="Trophoblast stem cell"  
/dev\_stage="3.5-dpc"  
/lab\_host="DH10B"  
/clone\_lib="NIA Mouse Trophoblast Stem Cell cDNA Library  
(long)"  
/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:  
NotI; Mouse cDNA project by the Laboratory of Genetics,  
National Institute on Aging (NIA), Intramural Research  
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is  
a long-transcript enriched cDNA library (Ref. Genome Res.  
11: 1553-1558 (2001)). [PMID: 11544199]. Total RNAs were  
obtained from Dr. Janet Rossant and Tilo Kunath (Samuel  
Lunenfeld Research Institute, Canada). Double-stranded  
cDNAs were synthesized with an Oligo(dT) primer  
[Invitrogen]:  
5'-pGACTAGTCTAGATCGCGCGCCCTTTT-3' from  
4 ug of total RNA, treated with T4 DNA polymerase, and  
purified by ethanol-precipitation. The cDNAs were ligated  
to lone-linker LU-Sal4, purified by phenol/chloroform, and  
separated from free linkers by Centricon 100. Then, the  
cDNAs were amplified by long-range high fidelity PCR using  
Ex Taq polymerase (Takara) with a primer Sal4-S. The  
products were purified by phenol/chloroform and Centricon  
100. The cDNAs were digested with SalI and NotI enzymes  
and cloned into SalI/NotI site of pSPORT1 plasmid vector.  
The DH10B E. coli host was transformed with the ligation  
mixture by the standard chemical method. The average  
insert size is about 2.6 kb. The library was constructed  
by Yulan Piao (NIA)."

**ORIGIN**

Query Match 91.1%; Score 16.4; DB 4; Length 674;  
Best Local Similarity 94.4%; Pred. No. 1.3e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGGTACTTGGCTG 18  
|||||

Db 547 ATGCTTGATCTTGGCTG 564  
|||||

**RESULT 24**

**BM206907** BM206907 684 bp mRNA linear EST 04-MAY-2001  
**LOCUS** NISC-iv16a09 w2 Soares NMBP2 Pituitary Mus musculus cDNA clone  
IMAGE:4317617 5', mRNA sequence.  
**DEFINITION** BM206907  
**ACCESSION** BM206907  
**VERSION** BM206907.1 GI:13955172  
**KEYWORDS** EST.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 684)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
**JOURNAL** Tumor Gene Index  
**COMMENT** Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 cDNA Library Preparation: M. Bento Soares Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
 DNA Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC)  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 info@image.llnl.gov  
 MGI:1598385  
 Plate: L1AM9222 row: B column: 18  
 Seq primer: T7 primer.

**FEATURES** Location/Qualifiers  
 source  
 1..684  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4317617"  
 /tissue\_type="pituitary gland"  
 /dev\_stage="embryo, 14 dpc"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="Soares NMBP2 pituitary"  
 /note="Organ: brain; Vector: pT7T3D-Pac; Site\_1: NotI;  
 Site\_2: EcoRI; 1st strand cDNA was primed with a NotI -  
 oligo(dT) primer  
 5'-AATCGAAGATTCGCGCGCGCGCTTTTCTTTTCTTTT-3';  
 double-stranded cDNA was ligated to EcoRI adaptors;  
 5'-AATCGCGACAGG-3' AND 5'-CCGCGCGCG-3' (Pharmacia),  
 digested with NotI and cloned into the NotI and EcoRI  
 sites of the pT7T3D-Paci vector. Library went through one  
 round of normalization, and was constructed in the  
 laboratory of M. Bento Soares (University of Iowa)."

**ORIGIN**  
 Query Match 91.1%; Score 16.4; DB 4; Length 684;  
 Best Local Similarity 94.4%; Pred. No. 1.3e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**QY** 1 ATGCTTGCTACTTGGCTG 18  
 |||||  
**Db** 518 ATGCTTGCTACTTGGCTG 501  
 |||||

**RESULT 25**  
**BG083217/c**  
**LOCUS** BG083217 696 bp mRNA linear EST 18-DEC-2003  
**DEFINITION** H3085G11-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone  
 H3085G11 5', mRNA sequence.  
**ACCESSION** BG083217.2 GI:40069994  
**VERSION** EST.  
**KEYWORDS** EST.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 696)  
 Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X.,  
 Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H.,  
 Wood,W.H. III, Becker,K.G. and Ko,M.S.H.  
 Genome-wide expression profiling of mid-gestation placenta and  
 embryo using a 15,000 mouse developmental cDNA microarray  
 Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)  
 20381348  
 10922068  
 On Jan 26, 2001 this sequence version replaced gi:12565785.  
 Other ESTs: H3085G11-3  
 Contact: George J. Kargul  
 Laboratory of Genetics  
 National Institute on Aging/National Institutes of Health  
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
**JOURNAL** Tumor Gene Index  
**COMMENT** Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 cDNA Library Preparation: M. Bento Soares Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
 DNA Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC)  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 info@image.llnl.gov  
 MGI:1598385  
 Plate: L1AM9222 row: B column: 18  
 Seq primer: T7 primer.

**FEATURES** Location/Qualifiers  
 source  
 1..696  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="CS7BL/6J"  
 /db\_xref="nlaEST:H3085G11-5"  
 /db\_xref="taxon:10090"  
 /clone="H3085G11"  
 /sex="Clones arrayed from a variety of cDNA libraries"  
 /dev\_stage="Clones arrayed from a variety of cDNA  
 libraries"  
 /lab\_host="DH10B"  
 /clone\_lib="NIA Mouse 15K cDNA Clone Set"  
 /note="Vector: pSPORT1; Site\_1: SalI; Site\_2: NotI; This  
 clone is among a rearranged set of 15,247 clones from 11  
 embryo cDNA libraries (including preimplantation stage  
 embryos from unfertilized egg to blastocyst, embryonic  
 part of E7.5 embryos, extraembryonic part of E7.5  
 embryos, and E12.5 female mesonephros/gonad) and one  
 newborn ovary cDNA library. Average insert size 1.5 Kb.  
 All source libraries are cloned unidirectionally with  
 Oligo(dT)-Not primers. References include: (1)  
 Genome-wide expression profiling of mid-gestation  
 placenta and embryo using a 15,000 mouse developmental  
 cDNA microarray, 2000, Proc. Natl. Acad. Sci. U.S.A. 97:  
 9127-9132; (2) Large-scale cDNA analysis reveals phased  
 gene expression patterns during preimplantation mouse  
 development, 2000, Development, 127: 1737-1749; (3)  
 Genome-wide mapping of unselected transcripts from  
 extraembryonic tissue of 7.5-day mouse embryos reveals  
 enrichment in the t-complex and under-representation on  
 the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

**ORIGIN**  
 Query Match 91.1%; Score 16.4; DB 4; Length 696;  
 Best Local Similarity 94.4%; Pred. No. 1.3e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**QY** 1 ATGCTTGCTACTTGGCTG 18  
 |||||  
**Db** 540 ATGCTTGCTACTTGGCTG 523  
 |||||

**RESULT 26**  
**BM951736/c**  
**LOCUS** BM951736 713 bp mRNA linear EST 14-MAR-2002  
**DEFINITION** UI-M-EGU-bup-1-03-0-UI-r1 NIH-BMAP\_EGO Mus musculus cDNA clone  
 IMAGE:5685266 5', mRNA sequence.  
**ACCESSION** BM951736  
**VERSION** BM951736.1 GI:19435313  
**KEYWORDS** EST.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 713)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Dr. James Lin, University of Iowa  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: MGC clone distribution information can be

Email: cdna@lgsun.grc.nia.nih.gov  
 This clone set has been freely distributed to the community. Please  
 visit <http://lgsun.grc.nia.nih.gov/cDNA/15k.html> for details.  
 Plate: H3085 row: G column: 11  
 Seq primer: -21M13 Reverse  
 High quality sequence stop: 696  
 POLYA=No.

## FEATURES

## source

Location/Qualifiers  
 1..696  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strains="CS7BL/6J"  
 /db\_xref="nlaEST:H3085G11-5"  
 /db\_xref="taxon:10090"  
 /clone="H3085G11"  
 /sex="Clones arrayed from a variety of cDNA libraries"  
 /dev\_stage="Clones arrayed from a variety of cDNA  
 libraries"  
 /lab\_host="DH10B"  
 /clone\_lib="NIA Mouse 15K cDNA Clone Set"  
 /note="Vector: pSPORT1; Site\_1: SalI; Site\_2: NotI; This  
 clone is among a rearranged set of 15,247 clones from 11  
 embryo cDNA libraries (including preimplantation stage  
 embryos from unfertilized egg to blastocyst, embryonic  
 part of E7.5 embryos, extraembryonic part of E7.5  
 embryos, and E12.5 female mesonephros/gonad) and one  
 newborn ovary cDNA library. Average insert size 1.5 Kb.  
 All source libraries are cloned unidirectionally with  
 Oligo(dT)-Not primers. References include: (1)  
 Genome-wide expression profiling of mid-gestation  
 placenta and embryo using a 15,000 mouse developmental  
 cDNA microarray, 2000, Proc. Natl. Acad. Sci. U.S.A. 97:  
 9127-9132; (2) Large-scale cDNA analysis reveals phased  
 gene expression patterns during preimplantation mouse  
 development, 2000, Development, 127: 1737-1749; (3)  
 Genome-wide mapping of unselected transcripts from  
 extraembryonic tissue of 7.5-day mouse embryos reveals  
 enrichment in the t-complex and under-representation on  
 the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 This clone was contributed by the Brain Molecular Anatomy Project  
 (BMAP)

Seq primer: pYX-5.

Location/Qualifiers

1. .713  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="CS7BL/6"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5685266"  
 /tissue\_type="whole brain"  
 /dev\_stage="embryo 18.5 dpc"  
 /lab\_host="DHI0B (T1 phage resistant)"  
 /clone\_lib="NIH\_BMAP\_EGO"

/note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCCACGAC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

#### ORIGIN

Query Match 91.1%; Score 16.4; DB 5; Length 713;  
 Best Local Similarity 94.4%; Pred. No. 1.3e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGCTACTTGCGCTG 18

|||||

Db 215 ATGCTTGCTACTTGCGCTG 198

#### RESULT 27

BU562448/c

LOCUS

DEFINITION AGENCOURT 10388665 NIH\_MGC\_144 Mus musculus cDNA clone

IMAGE:6594214 5', mRNA sequence.

ACCESSION BU562448

VERSION BU562448.1

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Dr. Michael Brownstein  
 cDNA Library Preparation: Michael Brownstein Laboratory  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

Plate: L1CM2820 row: d column: 22

High quality sequence stop: 563.

Location/Qualifiers

1. .718  
 /organism="Mus musculus"  
 /mol\_type="mRNA"

#### FEATURES

source

/db\_xref="taxon:10090"  
 /clone="IMAGE:6594214"  
 /lab\_host="DHI0B (T1-phage-resistant)"  
 /clone\_lib="NIH\_MGC\_144"  
 /note="Organ: Brain; Vector: pDNR-LIB; Site 1: SfiI  
 (ggccattatggcc); Site 2: SfiI (ggcgcctggcc); cDNA made  
 by oligo-dT priming and directionally cloned. 5' and 3'  
 adaptors were used in cloning as follows:  
 5'-AAGCAGTGTATACACGAGATGGCCATTACGCCGGG-3' and  
 5'-ATTCTAGAGCGGCGGCGGACATG-DT(30)NN-3'. Full-length  
 enriched library was constructed using the Clontech  
 Creator SMART kit and size-selected to contain the 0.2-0.5  
 kb size fraction (other fractions present in NIH\_MGC\_143).  
 Library created in the laboratory of M. Brownstein (NIMH,  
 NIH). Note: this is a NIH\_MGC Library."

#### ORIGIN

Query Match 91.1%; Score 16.4; DB 5; Length 718;

Best Local Similarity 94.4%; Pred. No. 1.3e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGCTACTTGCGCTG 18

|||||

Db 137 ATGCTTGCTACTTGCGCTG 120

#### RESULT 28

CF725178/c

LOCUS

DEFINITION

UI-M-G20-cjo-j-17-0-UI-r1 NIH\_BMAP\_G20 Mus musculus cDNA clone

IMAGE:30606088 5', mRNA sequence.

ACCESSION CF725178

VERSION CF725178.1

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Dr. James Lin University of Iowa

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

<http://genome.uiowa.edu/distribution/mousefi.html>

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seq primer: pYX-5.

Location/Qualifiers

1. .718

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="CS7BL/6"

/db\_xref="taxon:10090"

/clone="IMAGE:30606088"

/tissue\_type="whole eye"

/dev\_stage="embryo 12.5-13.5, 14.5 dpc"

/lab\_host="DHI0B (T1 phage resistant)"

/clone\_lib="NIH\_BMAP\_G20"

/note="Organ: Eye; Vector: pYX-Asc; Site 1: EcoR I;

Site 2: Not I; The library was constructed according

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured RNA was size fractionated on a 1% agarose

gel. First strand cDNA synthesis was primed with oligo-dT

primer containing a Not I site. Double strand cDNA was

size selected according to mRNA size fraction, ligated

with EcoR I adaptor, digested with NotI and then cloned

directionally into pYX-Asc vector. The library tag

directionally into pYX-Asc vector. The library tag

sequence located between the Not I site and the polyA tail is TTATGAGT. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

## ORIGIN

Query Match 91.1%; Score 16.4; DB 7; Length 718;  
Best Local Similarity 94.4%; Pred. No. 1.3e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGCTTGACTTGCTG 18  
|||||  
Db 220 ATGCTTGACTTGCTG 203  
|||||

## RESULT 29

BU05577/c  
LOCUS  
DEFINITION BU05577 727 bp mRNA linear EST 26-AUG-2002  
IMAGE:6406689 5', mRNA sequence.

ACCESSION BU05577

VERSION BU05577.1 GI:22495654

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 727)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seq primer: pYX-5.

Location/Qualifiers

1..727

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6"

/db\_xref="taxon:10090"

/clone="IMAGE:6406689"

/tissue\_type="whole brain"

/dev\_stage="embryo 12.5dpc"

/lab\_host="DH10B (T1 phage resistant)"

/clone\_lib="NIH BMAP FOO"

/note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;

Site 2: Not I; The library was constructed according

Bonaldi, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured RNA was size fractionated on a 1% agarose

gel. First strand cDNA synthesis was primed with oligo-dr

primer containing a Not I site. Double strand cDNA was

size selected according to mRNA size fraction, ligated

with EcoR I adaptor, digested with NotI and then cloned

directionally into pYX-Asc vector. The library tag

sequence located between the Not I site and the polyA tail

is TGAGAGACC. This library was created for the University

Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the

Developing Mouse Nervous System', supported by National

Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,

## ORIGIN

Query Match 91.1%; Score 16.4; DB 5; Length 727;  
Best Local Similarity 94.4%; Pred. No. 1.3e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGCTTGACTTGCTG 18  
|||||  
Db 386 ATGCTTGACTTGCTG 369  
|||||

## RESULT 30

AG305472/c

LOCUS

DEFINITION AG305472 730 bp DNA linear GSS 02-JUN-2004

sequence.

ACCESSION AG305472

VERSION AG305472.1 GI:47878426

KEYWORDS GSS.

SOURCE Mus musculus molossinus

ORGANISM Mus musculus molossinus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 730)

Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

BAC end Sequences of Library MSMg01

Unpublished

2 (bases 1 to 730)

Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

Direct Submission

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehito-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

(E-mail: [hattori@psc.riken.jp](mailto:hattori@psc.riken.jp), URL: <http://hgp.gsc.riken.go.jp/>,

Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC

library availability, please contact Kuniya Abe ([abe@rtc.riken.jp](mailto:abe@rtc.riken.jp)).

Tsukuba Institute, Bio Resource Center,

The Institute of Physical and Chemical Research (RIKEN) 3-1-1

Kovadai, Tsukuba, 305-0074 Japan

Phone: 81-298-36-9189, fax: 81-298-36-9199

e-mail: [abe@rtc.riken.jp](mailto:abe@rtc.riken.jp)

PRIMERS

Sequencing : T7

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI.

Location/Qualifiers

1..730

/organism="Mus musculus molossinus"

/mol\_type="genomic DNA"

/sub\_species="molossinus"

/db\_xref="taxon:57488"

/clone="MSMg01-086A23.T7"

/sex="male"

/tissue\_type="mixture of kidney and spleen"

/clone\_lib="MSMg01 Mouse Male BAC Library"

ORIGIN

Query Match 91.1%; Score 16.4; DB 9; Length 730;

Best Local Similarity 94.4%; Pred. No. 1.3e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGACTTGCTG 18

|||||

Db 651 ATGCTTGACTTGCTG 634

|||||

RESULT 31

CF520490/c

LOCUS

DEFINITION CF520490 750 bp mRNA linear EST 10-SEP-2003

AGENCOURT 15508932 NICHG\_XGC\_Kid1 Xenopus laevis cDNA clone

IMAGE:7008569 5', mRNA sequence.

ACCESSION CF520490

VERSION CF520490.1 GI:34570346  
 KEYWORDS EST.  
 SOURCE Xenopus laevis (African clawed frog)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 Xenopodinae; Xenopus; Xenopus.  
 REFERENCE 1 (bases 1 to 750)  
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgapsb-r@mail.nih.gov  
 Tissue Procurement: Dr. Igor David  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone Distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L1AM14712 row: i column: 15  
 High quality sequence stop: 635.  
 FEATURES  
 source  
 Location/Qualifiers  
 1..750  
 /organism="Xenopus laevis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8355"  
 /clone="IMAGE:7008569"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NICHD\_XGC\_Kidl"  
 /note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.  
 Average insert size 2.2 kb. Constructed by Life  
 Technologies. Note: This is a Xenopus Gene Collection  
 (XGC) library."  
 ORIGIN  
 Query Match 91.1%; Score 16.4; DB 7; Length 750;  
 Best Local Similarity 94.4%; Pred. No. 1.3e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 ATGCTTGGTACTTGGCTG 18  
 |||||||  
 Db 494 ATGCTTGGTCTTGGCTG 477  
 RESULT 32  
 CF732338/c  
 LOCUS  
 DEFINITION UI-M-G20-cj-r-h-03-0-UI.r1 NIH BMAP\_G20 Mus musculus cDNA clone  
 IMAGE:30603722 5', mRNA sequence.  
 CF732338  
 VERSION CF732338.1 GI:37628671  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 765)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapsb-r@mail.nih.gov  
 Tissue Procurement: Dr. James Lin University of Iowa  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Distribution information can be found at

<http://genome.uiowa.edu/distribution/mousef1.html>  
 This clone was contributed by the Brain Molecular Anatomy Project  
 (BMAP)  
 Seq primer: pYX-5.  
 FEATURES  
 source  
 Location/Qualifiers  
 1..765  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:30603722"  
 /tissue\_type="whole eye"  
 /dev\_stage="embryo 12.5,13.5,14.5 dpc"  
 /lab\_host="DH10B (T1 phage resistant)"  
 /clone\_lib="NIH BMAP\_G20"  
 /note="Organ: Eye; Vector: pYX-Asc; Site 1: EcoR I;  
 Site 2: Not I; The library was constructed according  
 Ronaldo, Lennon and Soares, Genome Research, 6:791-806,  
 1996. Denatured RNA was size fractionated on a 1% agarose  
 gel. First strand cDNA synthesis was primed with oligo-dT  
 primer containing a Not I site. Double strand cDNA was  
 size selected according to mRNA size fraction, ligated  
 with EcoR I adaptor, digested with NotI and then cloned  
 directionally into pYX-Asc vector. The library tag  
 sequence located between the Not I site and the polyA tail  
 is TTATTGAAGT. This library was created for the University  
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
 Developing Mouse Nervous System', supported by National  
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,  
 program coordinator."  
 ORIGIN  
 Query Match 91.1%; Score 16.4; DB 7; Length 765;  
 Best Local Similarity 94.4%; Pred. No. 1.3e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 ATGCTTGGTACTTGGCTG 18  
 |||||||  
 Db 93 ATGCTTGATCTTGGCTG 76  
 RESULT 33  
 CO815137  
 LOCUS  
 DEFINITION AGENCOURT 30258527 NIH MGC 257 Mus musculus cDNA clone  
 IMAGE:30931439 5', mRNA sequence.  
 CO815137  
 VERSION CO815137.1 GI:51033768  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 803)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgapsb-r@mail.nih.gov  
 Tissue Procurement: Dr. Kathleen Horner, Stanford University  
 cDNA Library Preparation: Express Genomics  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: NDAM1179 row: b column: 24  
 High quality sequence stop: 547.  
 FEATURES  
 source  
 Location/Qualifiers  
 1..803

/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:30931439"  
/lab\_host="DH10B Tona"  
/clone\_lib="NIH\_MGC\_257"  
/note="Organ: oocyte; Vector: pExpress-1; Site:1: EcoRV;  
Site 2: NotI; cDNA was primed using oligo-dt primer:  
5'-P-GA-TAGTCTAGATCGAGCCGCC(T)25-3' and cloned into  
the EcoRV/NotI sites of pExpress-1. Size-selection >0.5 kb  
resulted in an average insert size of 1.0kb. This is a  
normalized library (primary library is NIH\_MGC\_256) and  
was constructed by Express Genomics (Frederick, MD). Note:  
this is a NIH\_MGC library"

## ORIGIN

Query Match 91.1%; Score 16.4; DB 7; Length 803;  
Best Local Similarity 94.4%; Pred. No. 1.3e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGCTTGCTACTGGCTG 18  
||||| |||||||  
Db 564 ATGCTTGCTACTGGCTG 581

RESULT 34  
CD301011/c  
LOCUS  
DEFINITION AGENCOURT\_14238470 NICHD\_XGC\_Eyel Xenopus laevis cDNA clone  
IMAGE:6957777 5', mRNA sequence.  
ACCESSION CD301011  
VERSION CD301011.1 GI:31080806  
KEYWORDS EST.  
SOURCE Xenopus laevis (African clawed frog)

ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
Xenopodinae; Xenopus; Xenopus.  
REFERENCE 1 (bases 1 to 845)  
NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-remail.nih.gov  
Tissue Procurement:  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLNL4587 row: a column: 08  
High quality sequence stop: 721.  
Location/Qualifiers  
1. .845

FEATURES  
source  
/organism="Xenopus laevis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
/clone="IMAGE:6957777"  
/dev\_stage="adult"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NICHD\_XGC\_Eyel"  
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 2.3 kb. Constructed by Life  
Technologies. Note: This is a Xenopus Gene Collection  
(XGC) library."

## ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 845;

Best Local Similarity 94.4%; Pred. No. 1.3e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGCTTGCTACTGGCTG 18  
||||| |||||||  
Db 524 ATGCTGGTACTGGCTG 507

RESULT 35  
BI690731/c  
LOCUS  
DEFINITION BI690731 NCI\_CGAP\_Mam6 Mus musculus cDNA clone IMAGE:5354218 5',  
mRNA sequence.  
ACCESSION BI690731  
VERSION BI690731.1 GI:15653360  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)

ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 880)  
NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Jeffrey Green M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLNL1900 row: j column: 11  
High quality sequence stop: 807.  
Location/Qualifiers  
1. .880

FEATURES  
source  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strains="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5354218"  
/sex="female, virgin"  
/tissue\_type="infiltrating ductal carcinoma"  
/dev\_stage="5 months"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Mam6"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Library constructed by Life Technologies. Investigator  
providing samples: Jeffrey Green, M.D., NIH"

ORIGIN  
Query Match 91.1%; Score 16.4; DB 4; Length 880;  
Best Local Similarity 94.4%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGCTTGCTACTGGCTG 18  
||||| |||||||  
Db 817 ATGCTTGATCTGGCTG 800

RESULT 36  
CC399964/c  
LOCUS  
DEFINITION PHS18478 ZM.0.6.1.0 KB Zea mays genomic clone ZMMBra523M23,  
genomic survey sequence.  
ACCESSION CC399964  
VERSION CC399964.1 GI:30880054  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;



Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

# REFERENCE

1 (bases 1 to 906)  
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and

Bennetzen, J.  
Maize Genomics Consortium  
Unpublished (2003)

Other GSSs: FUS184TD  
Contact: Cathy Whitelaw

TIGR  
Seq primer: TR

Class: sheared ends.  
Location/Qualifiers  
1..906

9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TR

Class: sheared ends.

FEATURES  
source

1..906

/organism="Zea mays"

/mol\_type="genomic DNA"

/strain="B73"

/db\_xref="taxon:4577"

/clone="ZMMBTa523M23"

/clone\_lib="ZM 0.6 1.0 KB"

/note="Vector: pCR4-ToPO; Site 1: EcoRI; 0.6-1.0 kb high

COT selected genomic DNA library"

# ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 906;

Best Local Similarity 94.4%; Pred. No. 1.4e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGCTACTTGCTG 18

Db 846 ATGCTTGCTACTTGCTG 829

# RESULT 37

CC399967 907 bp DNA linear GSS 19-MAY-2003

LOCUS FUS184TD ZM\_0.6 1.0 KB Zea mays genomic clone ZMMBTa523M23,

DEFINITION genomic survey sequence.

CC399967

CC399967.1 GI:30880057

GSS.

Ze mays

Ze mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 907)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and

Bennetzen, J.

Maize Genomics Consortium

Unpublished (2003)

Other GSSs: FUS184TB

Contact: Cathy Whitelaw

TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TR

Class: sheared ends.

FEATURES  
source

1..907

/organism="Zea mays"

/mol\_type="genomic DNA"

/strain="B73"

/db\_xref="taxon:4577"

/clone="ZMMBTa523M23"

/clone\_lib="ZM 0.6 1.0 KB"

/note="Vector: pCR4-ToPO; Site 1: EcoRI; 0.6-1.0 kb high

COT selected genomic DNA library"

# ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 907;

Best Local Similarity 94.4%; Pred. No. 1.4e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGCTACTTGCTG 18

Db 493 ATGCTTGCTACTTGCTG 510

# RESULT 38

AK013315/c

LOCUS

DEFINITION

AK013315

AK013315.1 GI:12850604

HTC; CAP trapper.

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

AK013315 938 bp mRNA linear HTC 03-APR-2004  
Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length  
enriched library, clone:2810449M14 product:inferred: RIKEN cDNA  
5730434B08 gene, full insert sequence.

AK013315

AK013315.1 GI:12850604

HTC; CAP trapper.

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

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MEDLINE

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JOURNAL

MEDLINE

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REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujitake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)

20530913

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

5

The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 938)

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,

Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,

Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,

Hirooka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M.,

Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,

Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,



Query Match 91.1%; Score 16.4; DB 6; Length 941;  
Best Local Similarity 94.4%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGACTTGGCTG 18  
DB 393 ATGCTTGACTTGGCTG 376

RESULT 40  
BY717391/c  
LOCUS  
DEFINITION  
musculus cDNA clone 5730434B08 5', mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)

REFERENCE  
AUTHORS  
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,  
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,  
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,  
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,  
Ciothia, C., Corbani, L.E., Cousins, S., Dalia, E., Dragani, T.A.,  
Fletcher, C.F., Forrest, A., Frazer, K.R., Gassner, T.,  
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,  
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,  
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,  
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,  
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,  
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,  
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,  
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,  
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,  
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,  
Verardo, R., Wagner, L., Wallestedt, C., Wang, Y., Watanabe, Y.,  
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yang, I.,  
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimin, A., Carninci, P.,  
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,  
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,  
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,  
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,  
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,  
Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel.: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,  
Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,  
Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,  
Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,  
Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,  
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Takami, M.,  
Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.  
Direct Submission  
Computational Analysis of Full-Length Mouse cDNAs Compared with  
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
10 (11), 1757-1771 (2000)  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site (http://genome.gsc.riken.go.jp) for  
further details.

FEATURES  
source  
Location/Qualifiers  
1. .949  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strains="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="5730434B08"  
/tissue\_type="whole body"  
/dev\_stage="8 days embryo"  
/clone\_lib="RIKEN full-length enriched, 8 days embryo  
whole body"

ORIGIN  
Query Match 91.1%; Score 16.4; DB 6; Length 949;  
Best Local Similarity 94.4%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGACTTGGCTG 18  
DB 663 ATGCTTGACTTGGCTG 646

RESULT 41  
CL079594/c  
LOCUS  
DEFINITION  
Xenopus tropicalis genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Xenopus tropicalis (western clawed frog)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
Xenopodinae; Xenopus; Silurana.

REFERENCE  
AUTHORS  
Kremetzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,  
Mardis, E. and Wilson, R.

TITLE  
JOURNAL  
COMMENT  
A physical map of the xenopus tropicalis genome  
Unpublished (2003)  
Contact: Richard K Wilson  
Genome Sequencing Center  
Washington University School of Medicine  
Email: submissions@watson.wustl.edu  
Insert Length: 175000 Std Error: 0.00  
Seq primer: RM1 TACGACTCATTAGGAGG  
Class: BAC ends  
High quality sequence start: 13  
High quality sequence stop: 790.

FEATURES  
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/strain="Nigerian frog"  
/db\_xref="taxon:8364"  
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/cell\_line="Stock 248 F7A2, inbred N7"

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/clone lib="CH216"
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BAC library"

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Best Local Similarity 94.4%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTGGCTG 18
    |||||
Db 687 ATGCTTGCTACTTGCTG 670

RESULT 42
CL017579/c
LOCUS
DEFINITION
CH216-2F20_Sp6.1 CH216 Xenopus tropicalis genomic clone CH216-2F20,
genomic survey sequence.
CL017579
ACCESSION
CL017579.1 GI:40459392
VERSION
GSS.
KEYWORDS
Xenopus tropicalis (western clawed frog)
SOURCE
Xenopus tropicalis
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE
1 (bases 1 to 1041)
Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E. and Wilson, R.,
A physical map of the xenopus tropicalis genome
Unpublished (2003)
CONTACT: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp6 ATTATGGTGACACTATAG
Class: BAC ends
High quality sequence start: 25
High quality sequence stop: 786.
Location/Qualifiers
1..1041
/organism="Xenopus tropicalis"
/mol_type="Genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-2F20"
/sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/notes=Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"

ORIGIN
Query Match          91.1%; Score 16.4; DB 9; Length 1041;
Best Local Similarity 94.4%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTGGCTG 18
    |||||
Db 748 ATGCTTGCTACTTGCTG 731

RESULT 43
CK166006/c
LOCUS
DEFINITION
FGAS050052 Triticum aestivum FGAS: TaLT7 Triticum aestivum CDNA,
mRNA sequence.
CK166006
ACCESSION
CK166006.1 GI:38998628
VERSION
EST.
KEYWORDS
Triticum aestivum (bread wheat)

```

```

Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 1167)
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,
Peniket, C., Roach, J.L. and Sathan, F.,
Functional Genomics of Abiotic Stress in Wheat and Canola Crops
Unpublished (2003)
CONTACT: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas.ests@usask.ca
This sequence is the direct result of the base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [63,731].
Plate: TaLT707 row: G column: 05.
Location/Qualifiers
1..1167
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Wheat line CI 14106"
/db_xref="taxon:4565"
/lab_host="DHS alpha"
/clone_lib="Triticum aestivum FGAS: TaLT7"
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subtractive hybridization) cDNA library from genotype
CI14106 cold hardened at 2 C for 21 days and 49 days
(equal amount of cDNA pooled together before subtraction,
tester) and subtracted against genotype CI14106
non-hardened (20 C) (driver). Nitro-pyrole anchored
oligo-dT priming and non-directional cloning."

ORIGIN
Query Match          91.1%; Score 15.4; DB 7; Length 1167;
Best Local Similarity 94.4%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTTGCTG 18
    |||||
Db 789 ATGCTTGCTACTTGCTG 772

RESULT 44
AK017613/c
LOCUS
DEFINITION
Mus musculus 8 days embryo whole body CDNA, RIKEN full-length
enriched library, clone:5730434B08 product:inferred: RIKEN CDNA
5730434B08 gene, full insert sequence.
AK017613
ACCESSION
AK017613.1 GI:12856943
VERSION
HTC; CAP trapper.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PUBMED
10349636
2
REFERENCE
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

```

```

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Inoue,K., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohata,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2418)
Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
Shukui,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.jp/) for further
details.
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues. First strand cDNA was primed with a primer
[5', GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse transcriptase
and subsequently enriched for full-length by cap-trapper. cDNA went
through one round of subtraction to Not = 100.0. Second strand cDNA
was prepared with the primer adapter of sequence [5',
GAGAGAGAGATCTCGAGTTAATTAATCCCCCCCCCC 3']. cDNA was cleaved
with BamHI and XhoI. Vector: a modified pBluescript KS(+) after
bulk excision from Lambda FLC 1. Cloning sites, 5' end: SalI; 3'
end: BamHI. Host: DH10B
Location/Qualifiers
1..2418
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="PANTOM_DB:5730434B08"
/db_xref="taxon:10090"

FEATURES
source
Query Match 88.9%; Score 16; DB 1; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTTGGTACTTGGC 16
|||||
Db 196 ATGCTTGGTACTTGGC 181
|||||

/misc_feature
1..2418
/clone="5730434B08"
/tissue_type="whole body"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stages="8 days embryo"
1..2418
/note="Inferred: RIKEN cDNA 5730434B08 gene
(UniGene|Mm.27918, evidence: UC)"

ORIGIN
Query Match 91.1%; Score 16.4; DB 3; Length 2418;
Best Local Similarity 94.4%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGGTACTTGGCTG 18
|||||
Db 663 ATGCTTGATCTTGGCTG 646
|||||

RESULT 45
AA791396/c 435 bp mRNA linear EST 20-FEB-2001
LOCUS
DEFINITION
Mesembryanthemum crystallinum (common iceplant)
AA791396.1 GI:2854351
VERSION
AA791396
KEYWORDS
Mesembryanthemum crystallinum
SOURCE
Mesembryanthemum crystallinum
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Aizoaceae; Mesembryanthemum.
1 (bases 1 to 435)
Cushman, J.C.
An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum
Unpublished (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T7
BACKWARD: T3
Plate: L0-2 row: C column: 10
Seq primer: M13 reverse
High quality sequence stop: 300.
Location/Qualifiers
1..435
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="L0-130"
/tissue_type="leaf"
/dev_stage="Six week old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 0 hours NaCl treatment"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI"

ORIGIN
Query Match 88.9%; Score 16; DB 1; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTTGGTACTTGGC 16
|||||
Db 196 ATGCTTGGTACTTGGC 181
|||||

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## RESULT 46

BY474829  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

## REFERENCE

AUTHORS

1 (bases 1 to 524)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,

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Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,

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Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,

Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,

Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,

Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,

Kurochin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,

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Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,

Ravasi, T., Reed, J.C., Reid, D.J., Reid, J., Ring, B.Z., Ringwald, M.,

Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,

Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,

Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,

Wells, C., Wilming, L.G., Wyshaw-Boris, A., Yanagisawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,

Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,

Itch, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

Contact: Yoshihide Hayashizaki

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The Institute of Physical and Chemical Research (RIKEN)

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Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,

Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,

Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,

Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,

Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and

Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN,  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.

Cells were provided by Drs. William J Pavan, Stacie Loftus, and  
 Denise Larson (Division of Intramural Research Genetic Disease  
 Research Branch National Human Genome Research Institute, National  
 Institutes of Health (NIH) Building: 49, Room #A82 49 Convent Drive  
 MSC 4472 Bethesda, Maryland U.S.A) whose assistance we gratefully  
 acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
 further details.

## FEATURES

## source

1. .524

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="G370010N10"

/cell\_type="B16 F10Y cells"

/clone\_lib="RIKEN full-length enriched, B16 F10Y cells"

## ORIGIN

Query Match 88.9%; Score 16; DB 5; Length 524;

Best Local Similarity 100.0%; Pred. No. 2e+03; 0;

Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1 ATGCTTGGTACTTGGC 16

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Db 132 ATGCTTGGTACTTGGC 147

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RESULT 47

BE037010/c

LOCUS

DEFINITION

BE037010

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BE037010

BE037010

BE037010.1

EST.

MESEMBRYANTHEMUM CRYSTALLINUM (COMMON ICEPLANT)

MESEMBRYANTHEMUM CRYSTALLINUM

EUKARYOTA; VIRIDIPHYTES; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Aizoaceae; Mesembryanthemum.

1 (bases 1 to 534)

Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M.,

Ferreira, H., Kawasaki, S., McCollough, A., Michalowski, C.B.,

Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.

Functional Genomics of Plant Stress Tolerance

Unpublished (2000)

Contact: Michalowski, C.B.

University of Arizona

Bio Sciences West room 513, Tucson, AZ 85721, USA

Tel: 520-621-7982

Fax: 520-621-1697

Email: cbm@u.arizona.edu.

Location/Qualifiers

1. .534

/organism="Mesembryanthemum crystallinum"

/mol\_type="mRNA"

/db\_xref="taxon:3544"

/tissue\_type="apical meristem and leaf primordia"

/dev stages="6 weeks"

/clone\_lib="MP"

/note="3 d 500mM NaCl"

ORIGIN

Query Match 88.9%; Score 16; DB 2; Length 534;

Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1 ATGCTTGGTACTTGGC 16

|||||

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Db      472 ATGCTTGCTACTTGGC 457

RESULT 48
BM302206/c
LOCUS   BM302206               535 bp      mRNA      linear      EST 22-JAN-2002
DEFINITION MCA046H01.23596 Ice plant Lambda Uni-Zap XR expression library, 0
hours NaCl treatment prescreened for removal of highly abundant
transcripts Mesembryanthemum crystallinum cDNA clone MCA046H01.5,
mRNA sequence.
ACCESSION BM302206
VERSION   BM302206.1 GI:18024581
KEYWORDS EST.
SOURCE   Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Alzooaceae; Mesembryanthemum.
1 (bases 1 to 535)
REFERENCE Cushman, J.C.
AUTHORS An expressed sequence tag database for the common ice plant,
TITLE Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 037 row: H column: 01
Seq primer: T3 20mer
High quality sequence stop: 535.
FEATURES
source
Location/Qualifiers
1..535
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCT037H01"
/tissue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression acid
library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase IV (5:30 PM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Library construction was performed
according to Stratagene's recommended protocol for the
Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN
Query Match 88.9%; Score 16; DB 6; Length 559;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTTGGC 16
|||
Db 158 ATGCTTGCTACTTGGC 143

RESULT 50
AI822261/c
LOCUS AI822261               565 bp      mRNA      linear      EST 20-FEB-2001
DEFINITION L0-704T3 Ice plant Lambda Uni-Zap XR expression library, 0 hours
NaCl treatment Mesembryanthemum crystallinum cDNA clone L0-704.5,
similar to Chlorophyll a/b-binding protein type I precursor
(AL049488) [Arabidopsis thaliana], mRNA sequence.
ACCESSION AI822261
VERSION   AI822261.1 GI:5442599
KEYWORDS EST.
SOURCE   Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Alzooaceae; Mesembryanthemum.
1 (bases 1 to 565)
REFERENCE Cushman, J.C.
AUTHORS An expressed sequence tag database for the common ice plant,
TITLE Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

Db      372 ATGCTTGCTACTTGGC 357

RESULT 49
CA840475/c
LOCUS CA840475               559 bp      mRNA      linear      EST 12-DEC-2002
DEFINITION MCT037H01.174045 Ice plant Lambda Uni-Zap XR expression library, 5
days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
(5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT037H01.5,
mRNA sequence.
ACCESSION CA840475
VERSION   CA840475.1 GI:26568240
KEYWORDS EST.
SOURCE   Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Alzooaceae; Mesembryanthemum.

1 (bases 1 to 559)

An expressed sequence tag database for the common ice plant,

Mesembryanthemum crystallinum

Unpublished (1997)

Contact: Cushman JC

Department of Biochemistry

University of Nevada

MS200, Reno, NV 89557-0014, USA

Tel: 775-784-1918

Fax: 775-784-1650

Email: jcushman@unr.edu

PCR Primers

FORWARD: T3 20mer

BACKWARD: T7 21mer

Plate: 037 row: H column: 01

Seq primer: T3 20mer

High quality sequence stop: 559.

Location/Qualifiers

1..559

/organism="Mesembryanthemum crystallinum"

/mol\_type="mRNA"

/db\_xref="taxon:3544"

/clone="MCT037H01"

/tissue\_type="leaf"

/dev\_stage="five-week-old"

/clone\_lib="Ice plant Lambda Uni-Zap XR expression acid

library, 5 days 0.5 M NaCl treatment, Crassulacean acid

metabolism, phase IV (5:30 PM)."

/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:

EcoRI; Site 2: XhoI; Library construction was performed

according to Stratagene's recommended protocol for the

Lambda UniZapXR vector and cDNA synthesis kit."

Query Match 88.9%; Score 16; DB 6; Length 559;

Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTTGGC 16

|||

Db 158 ATGCTTGCTACTTGGC 143

RESULT 50

AI822261/c

LOCUS AI822261

DEFINITION L0-704T3 Ice plant Lambda Uni-Zap XR expression library, 0 hours

NaCl treatment Mesembryanthemum crystallinum cDNA clone L0-704.5,

similar to Chlorophyll a/b-binding protein type I precursor

(AL049488) [Arabidopsis thaliana], mRNA sequence.

ACCESSION AI822261

VERSION AI822261.1 GI:5442599

KEYWORDS EST.

SOURCE Mesembryanthemum crystallinum (common iceplant)

ORGANISM Mesembryanthemum crystallinum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Alzooaceae; Mesembryanthemum.

1 (bases 1 to 565)

Cushman, J.C.

An expressed sequence tag database for the common ice plant,

Mesembryanthemum crystallinum

Unpublished (1997)

Contact: Cushman JC

Department of Biochemistry

University of Nevada

MS200, Reno, NV 89557-0014, USA

Tel: 775-784-1918

Fax: 775-784-1650

Email: jcushman@unr.edu

PCR Primers  
 FORWARD: T7  
 BACKWARD: T3  
 Plate: LO-8 row: B column: 8  
 Seq primer: T3  
 High quality sequence stop: 400.

## FEATURES

Location/Qualifiers  
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 /organism="Mesembryanthemum crystallinum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3544"  
 /clone="LO-704"  
 /tissue\_type="Leaf"  
 /dev\_stage="Six week old"  
 /clone\_lib="Ice plant Lambda Uni-Zap XR expression  
 library, 0 hours NaCl treatment"  
 /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site\_1:  
 EcoRI; Site\_2: XhoI"

## ORIGIN

Query Match 88.9%; Score 16; DB 1; Length 565;  
 Best Local Similarity 100.0%; Pred.No. 2e+03;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTTGGC 16  
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 Db 469 ATGCTTGCTACTTGGC 454

Search completed: December 3, 2004, 05:50:46  
 Job time : 2348.45 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 2, 2004, 20:35:25 ; Search time 257.211 Seconds  
(without alignments)  
367.363 Million cell updates/sec

US-10-050-189a-9

Title: Perfect score: 18  
Sequence: 1 atgcttggtactggctg 18

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : N\_Geneseq\_23Sep04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6 ABN84787	Abn84787 Primer us
2	18	100.0	66479	6 ABQ80567	Abq80567 Mutant hu
3	18	100.0	66479	6 ABQ80566	Abq80566 Mutant hu
4	18	100.0	66479	6 ABQ80568	Abq80568 Mutant hu
5	18	100.0	66479	6 ABQ80565	Abq80565 Human IKB
6	16.4	91.1	201	10 ACF67663	Acf67663 Photorhab
7	16.4	91.1	751	10 ACF65423	Acf65423 Photorhab
8	16.4	91.1	1122	9 ADA31773	Ada31773 DNA encod
9	16.4	91.1	13629	4 ABL06290	Ab106290 Drosophil
10	16.4	91.1	110000	10 ACF65383_1	Continuation (2 of
11	16.4	91.1	110000	10 ACF65383_2	Continuation (3 of
12	15.4	85.6	1074	6 ABN62291	Abn62291 Streptoco
13	15.4	85.6	3045	10 ACF71824	Acf71824 Photorhab
14	15.4	85.6	15382	8 ACD13393	Adc13393 Human DNA
15	15.4	85.6	110000	10 ACF67367_50	Continuation (51 o
16	15.4	85.6	110000	10 ACF65387_1	Continuation (2 of
17	15.4	85.6	110000	10 ACF65387_2	Continuation (3 of
18	15.4	85.6	112414	6 ABL59091	Ab159091 Nucleotid
19	15.4	85.6	127432	12 ADO343653	Ado343653 Nucleotid
20	15.4	85.6	270150	11 ADP65796	Adp65796 Human 16p
21	15.4	85.6	271990	10 ADD25213	Add25213 Fertility

22	15.4	85.6	271990	12 ADN61228	Adn61228 Radish nu
23	15.4	85.6	349381	10 ADC87619	Adc87619 Human GPC
24	15	83.3	740	4 RAI196634	Rai196634 Human neu
25	15	83.3	873	6 ACA48194	Aca48194 Prokaryot
26	15	83.3	884	4 AAH05175	Aah05175 Human cDN
27	15	83.3	2351	10 ADE86815	Ade86815 Petunia P
28	15	83.3	2418	4 AAH15761	Aah15761 Human cDN
29	15	83.3	2444	3 AAC56059	Aac56059 Eucalyptu
30	15	83.3	2988	6 AD07786	Ado7786 Human sec
31	15	83.3	2988	6 AD07786	Ado7786 Human sec
32	15	83.3	3283	6 AD34069	Ad34069 Human sec
33	15	83.3	3283	6 AD34069	Ad34069 Human sec
34	15	83.3	3283	6 AD34069	Ad34069 Human sec
35	15	83.3	3616	5 ABA17709	Abal7709 Human ner
36	15	83.3	4584	5 ABV23436	Abv23436 Human pro
37	15	83.3	5170	5 ADL45673	Adl45673 Human ova
38	15	83.3	7120	4 ABL04480	Ab104480 Drosophil
39	15	83.3	183610	8 ACF62736	Acf62736 Cancer ba
40	15	83.3	183610	8 ACF62736	Acf62736 Cancer ba
41	15	83.3	183610	10 ADB87940	Adb87940 Human UGT
42	15	83.3	183610	10 ADB87940	Adb87940 Human UGT
43	15	83.3	183610	10 ADB96923	Adb96923 Human MDR
44	14.8	82.2	192	11 ACH97379	Ach97379 Klebsiell
45	14.8	82.2	225	10 ADF57719	Adf57719 Human col
46	14.8	82.2	449	4 AHA34718	Aah34718 Human col
47	14.8	82.2	575	12 ACH72550	Ach72550 Human gen
48	14.8	82.2	585	4 ABA09266	Abao9266 Human sec
49	14.8	82.2	597	5 AAS05467	Aas05467 Mammalian
50	14.8	82.2	657	10 ACF71365	Acf71365 Photorhab
51	14.8	82.2	681	4 ABL18361	Ab118361 Drosophil
52	14.8	82.2	847	4 ABL12051	Ab112051 Drosophil
53	14.8	82.2	1116	6 ABN90844	Abn90844 Staphyloc
54	14.8	82.2	1156	12 ADJ42190	Adj42190 Plant cDN
55	14.8	82.2	1242	10 ADF01578	Adf01578 Bacterial
56	14.8	82.2	1467	12 ADL12786	Adl12786 Human ste
57	14.8	82.2	1497	10 ABZ39547	Abz39547 N. gonorr
58	14.8	82.2	1497	10 ABZ39547	Abz39547 N. gonorr
59	14.8	82.2	1638	6 ADA44508	Aad44508 A. variab
60	14.8	82.2	1959	4 AAF3081	Aaf3081 Human sec
61	14.8	82.2	1959	12 ABE267123	Abz67123 Human sec
62	14.8	82.2	2094	12 ADL03995	Adl03995 DNA encod
63	14.8	82.2	2449	6 ABS70004	Abs70004 DNA seque
64	14.8	82.2	2453	6 ABS69976	Abs69976 Aspergill
65	14.8	82.2	2463	6 ABS70005	Abs70005 Aspergill
66	14.8	82.2	2466	6 ABN79775	Abn79775 Fungal ZB
67	14.8	82.2	2466	6 ABS69975	Abs69975 Aspergill
68	14.8	82.2	2494	4 AAS35988	Aas35988 Human car
69	14.8	82.2	2494	10 ADE46682	Ade46682 Human car
70	14.8	82.2	2526	6 ABS70002	Abs70002 DNA seque
71	14.8	82.2	2532	6 ABS70003	Abs70003 DNA seque
72	14.8	82.2	2743	4 ABL18360	Ab118360 Drosophil
73	14.8	82.2	2900	4 ABL12050	Ab112050 Drosophil
74	14.8	82.2	5348	4 ABL02884	Ab102884 Drosophil
75	14.8	82.2	5884	4 ABL25844	Ab125844 Drosophil
76	14.8	82.2	6196	4 ABL20074	Ab120074 Drosophil
77	14.8	82.2	12068	10 ADB67032	Adb67032 Mouse Gal
78	14.8	82.2	17386	9 ADB16930	Adb16930 Human DYX
79	14.8	82.2	17998	10 ADB67031	Adb67031 Mouse Gal
80	14.8	82.2	17998	10 ADB67031	Adb67031 Mouse Gal
81	14.8	82.2	18698	10 ADB67026	Adb67026 Mouse Gal
82	14.8	82.2	25973	10 ADB67041	Adb67041 Mouse Gal
83	14.8	82.2	28534	10 ADB67028	Adb67028 Mouse Gal
84	14.8	82.2	30889	4 ABL19852	Ab119852 Drosophil
85	14.8	82.2	31563	4 ABL02738	Ab102738 Drosophil
86	14.8	82.2	32184	4 AAL05850	Aal05850 Human rep
87	14.8	82.2	32184	4 AAL05850	Aal05850 Human rep
88	14.8	82.2	32204	4 AAL05849	Aal05849 Human rep
89	14.8	82.2	32204	4 AAL05849	Aal05849 Human rep
90	14.8	82.2	36221	4 AAS00624	Aas00624 Human dea
91	14.8	82.2	38189	4 ABL19856	Ab119856 Drosophil
92	14.8	82.2	39814	4 ABL19854	Ab119854 Drosophil
93	14.8	82.2	103841	6 ABT00010_14	Continuation (15 o
94	14.8	82.2	103841	6 ABT01503_14	Continuation (15 o

95	14.8	82.2	103841	12	ADH77486_14	Continuation (15 o	14.4	80.0	8617	4	AAK52052	Aak52052 Human pol
96	14.8	82.2	103900	4	AAK95240_14	Continuation (15 o	14.4	80.0	28660	4	ABL09700	AbL09700 Drosophila
97	14.8	82.2	103900	4	AAK96733_14	Continuation (15 o	14.4	80.0	58909	4	AAF28543	Aaf28543 Genomic f
98	14.8	82.2	110000	10	ACF67367_45	Continuation (46 o	14.4	80.0	99014	6	ABN96931	Abn96931 Gene #342
99	14.8	82.2	110000	10	ACF65388_02	Continuation (3 of	14.4	80.0	110000	9	ADB12064_04	ADB12064 Gene #5 of
100	14.8	82.2	110000	12	ADQ79173_1	Continuation (2 of	14.4	80.0	110000	9	ADB12064_05	ADB12064 Gene #6 of
101	14.8	82.2	115863	12	ADQ19685_1	Adq19685 Human sof	14.4	80.0	142519	10	AA54634	Aa54634 Human chr
102	14.8	82.2	115211	4	AAF28553	Aaf28553 Genomic f	14.4	77.8	24	6	AB552843	Ab552843 Typha lat
103	14.8	82.2	163319	3	AAF22306	Aaf22306 Arabidops	14.4	77.8	24	10	AA62718	Aa62718 Typha lat
104	14.8	82.2	170834	10	AAAD22833	Aad22833 Human BAC	14.4	77.8	31	2	AA338573	Aa338573 Human gen
105	14.4	80.0	246	6	ABN46144	Abn46144 Human spl	14.4	77.8	227	2	AA410749	Aa410749 Human bla
106	14.4	80.0	246	6	ABK64679	Abk64679 Human ben	14.4	77.8	253	3	AAA41894	Aaa41894 Human sec
107	14.4	80.0	273	5	ABN16022	Abn16022 Human ORF	14.4	77.8	383	10	ABT41676	Abt41676 Toxicity
108	14.4	80.0	348	5	AA64815	Aa64815 DNA encod	14.4	77.8	436	5	AAF66073	Aaf66073 Novel hum
109	14.4	80.0	348	5	AA88997	Aa88997 DNA encod	14.4	77.8	510	3	AA533855	Aa533855 Arabidops
110	14.4	80.0	370	9	ACH50296	Ach50296 Human leu	14.4	77.8	553	9	ACH36414	Ach36414 Human end
111	14.4	80.0	454	9	ACH40660	Ach40660 Human foe	14.4	77.8	829	3	AA36344	Aa36344 Arabidops
112	14.4	80.0	471	10	ADF58467	Adf58467 Human pol	14.4	77.8	838	5	ABV11481	Abv11481 Human pro
113	14.4	80.0	473	4	AD051100	Ad051100 Human sec	14.4	77.8	933	9	ADB11893	Abd11893 Alloiooc
114	14.4	80.0	477	6	ABK78278	Abk78278 Bacillus	14.4	77.8	933	6	AB215187	Ab215187 Arabidops
115	14.4	80.0	502	12	ACH75781	Ach75781 Human gen	14.4	77.8	1197	4	ABL29887	AbL29887 Drosophila
116	14.4	80.0	534	12	ACH7284	Ach7284 Human gen	14.4	77.8	1895	4	AAH95561	Aah95561 Human pro
117	14.4	80.0	547	10	ADD27452	Add27452 Human adi	14.4	77.8	1935	3	AA57879	Aa57879 Seneciolo
118	14.4	80.0	548	10	ADD27579	Add27579 Human adi	14.4	77.8	2010	10	ADC08564	Adc08564 Rice DNA
119	14.4	80.0	557	6	ABQ98859	Abq98859 Human ORF	14.4	77.8	2069	3	AAZ50929	Aaz50929 Human pro
120	14.4	80.0	603	4	AA531453	Aa531453 Human CDN	14.4	77.8	2174	10	ABT31926	Abt31926 Human bre
121	14.4	80.0	603	6	ABQ66777	Abq66777 Human pol	14.4	77.8	2178	6	ABN59780	Abn59780 Novel hum
122	14.4	80.0	603	10	ADC10799	Adc10799 Human CDN	14.4	77.8	2418	6	AB552841	Ab552841 Typha lat
123	14.4	80.0	771	12	ACH90985	Ach90985 Human gen	14.4	77.8	2418	10	AA62716	Aa62716 Typha lat
124	14.4	80.0	782	3	AA531166	Aa531166 Arabidops	14.4	77.8	2842	4	AA533116	Aa533116 DNA encod
125	14.4	80.0	792	6	ABK75684	Abk75684 Bacillus	14.4	77.8	3015	4	AAH16309	Aah16309 Human CDN
126	14.4	80.0	804	8	ACA39084	Aca39084 Prokaryot	14.4	77.8	3076	8	ABT19951	Abt19951 Aspergill
127	14.4	80.0	831	12	ADL02758	Adl02758 DNA encod	14.4	77.8	3076	8	ABT18137	Abt18137 Aspergill
128	14.4	80.0	1014	10	ADB69722	Adb69722 C. neofo	14.4	77.8	3167	12	ADJ48317	Adj48317 Maize oil
129	14.4	80.0	1106	6	ABN98330	Abn98330 Arabidops	14.4	77.8	6276	4	ABL29886	AbL29886 Drosophila
130	14.4	80.0	1423	12	ADI45164	Adi45164 Rice isop	14.4	77.8	78785	10	AAAL60948	Aal60948 Human nep
131	14.4	80.0	1450	10	ADB69361	Adb69361 C. neofo	14.4	77.8	110000	6	ABR03041_24	Continuation (25 o
132	14.4	80.0	1517	4	ABL23739	AbL23739 Drosophila	14.4	77.8	110000	9	ADB12064_13	Continuation (14 o
133	14.4	80.0	1539	9	ABD08013	Abd08013 Alloiooc	13.8	76.7	30	12	ADP09472	Adp09472 PCR prime
134	14.4	80.0	1539	9	ABD08011	Abd08011 Alloiooc	13.8	76.7	63	2	AAQ25305	Aaq25305 Encodes s
135	14.4	80.0	1631	10	ADF99546	Adf99546 Barley sa	13.8	76.7	80	12	ADM96197	Adm96197 Rat anti
136	14.4	80.0	1667	4	AA531348	Aa531348 Human pol	13.8	76.7	109	4	AAI21264	Aai21264 Probe #11
137	14.4	80.0	1667	6	ABQ66672	Abq66672 Human gen	13.8	76.7	109	4	ABR66346	AbR66346 Human foe
138	14.4	80.0	1667	10	ADC10694	Adc10694 Human CDN	13.8	76.7	109	4	AAI46535	Aai46535 Probe #15
139	14.4	80.0	1676	10	ADE62521	Ad62521 Rat gene	13.8	76.7	109	4	ABA48440	AbA48440 Human bre
140	14.4	80.0	2000	12	ADJ11128	Adj11128 Plant CDN	13.8	76.7	109	4	ABA33406	AbA33406 Probe #11
141	14.4	80.0	2091	11	ADJ11547	Adj11547 Rice DNA	13.8	76.7	109	4	AAK40502	Aak40502 Human bon
142	14.4	80.0	2101	4	AAH24245	Aah24245 Human oxi	13.8	76.7	109	4	AAK14763	Aak14763 Human bra
143	14.4	80.0	2113	4	AA931328	Aa931328 Human pol	13.8	76.7	109	4	ABS40065	AbS40065 Human liv
144	14.4	80.0	2158	10	ADA53909	Ada53909 Human cod	13.8	76.7	109	5	AAI06968	Aai06968 Probe #69
145	14.4	80.0	2165	12	ADNA1652	Adna1652 Novel hum	13.8	76.7	109	6	ABS14487	AbS14487 Human gen
146	14.4	80.0	2165	12	ADNA1650	Adna1650 Novel hum	13.8	76.7	183	10	ADH82520	Adh82520 Enterococ
147	14.4	80.0	2166	12	ADNA1649	Adna1649 Novel hum	13.8	76.7	207	3	AAH82125	Aah82125 Rat diff
148	14.4	80.0	2496	6	ABZ11990	Abz11990 Human pol	13.8	76.7	255	5	AAH82125	Aah82125 Rat diff
149	14.4	80.0	2496	6	ADMA4508	Adma4508 Novel hum	13.8	76.7	256	3	AAZ58203	Aaz58203 Corn phos
150	14.4	80.0	2945	5	AA513671	Aa513671 cDNA sequ	13.8	76.7	256	10	ABX93271	Abx93271 Corn EST
151	14.4	80.0	3133	10	ADA53992	Ada53992 Human cod	13.8	76.7	258	3	AAE11036	Aae11036 Fuesarium
152	14.4	80.0	3192	3	AAAC49328	Aac49328 Arabidops	13.8	76.7	259	3	AAZ58201	Aaz58201 Corn phos
153	14.4	80.0	3450	10	ADB69000	Adb69000 C. neofo	13.8	76.7	259	10	ABX93269	Abx93269 Corn EST
154	14.4	80.0	3820	4	ABL23738	AbL23738 Drosophila	13.8	76.7	262	3	AAZ58202	Aaz58202 Corn phos
155	14.4	80.0	3893	4	ABL20986	AbL20986 Drosophila	13.8	76.7	262	10	ABX93270	Abx93270 Corn EST
156	14.4	80.0	4670	4	AAK53036	Aak53036 Human pol	13.8	76.7	267	3	AAZ58195	Aaz58195 Corn phos
157	14.4	80.0	5121	10	AAAD54635	Aad54635 Human chr	13.8	76.7	267	10	ABX93263	Abx93263 Corn EST
158	14.4	80.0	5123	10	ADF76362	Adf76362 Novel hum	13.8	76.7	274	10	ABX83379	Abx83379 Corn ear-
159	14.4	80.0	5123	10	AAAD54636	Aad54636 Human chr	13.8	76.7	276	6	ABL73008	AbL73008 Corn tass
160	14.4	80.0	5526	6	ADH32210	Adh32210 Yeast sma	13.8	76.7	281	3	AAZ58208	Aaz58208 Corn phos
161	14.4	80.0	5763	4	ABL24646	AbL24646 Drosophila	13.8	76.7	281	10	ABX93276	Abx93276 Corn EST
162	14.4	80.0	5891	6	ABQ76356	Abq76356 S. cerevi	13.8	76.7	289	3	AAZ58204	Aaz58204 Corn phos
163	14.4	80.0	6110	8	ABZ74187	Abz74187 Secreted	13.8	76.7	289	10	ABX93272	Abx93272 Corn EST
164	14.4	80.0	6110	8	ADA98716	Ada98716 Human sec	13.8	76.7	291	10	ABX87591	Abx87591 Corn ear-
165	14.4	80.0	6110	10	ABZ67753	Abz67753 Human sec	13.8	76.7	297	3	AAZ58206	Aaz58206 Corn phos
166	14.4	80.0	7545	5	AA573907	Aa573907 DNA encod	13.8	76.7	297	3	AAZ58206	Aaz58206 Corn EST
167	14.4	80.0	7998	4	AAK79404	Aak79404 Human imm	13.8	76.7	301	12	ADG99781	Adg99781 Kidney di

C 241	13.8	76.7	324	4	AAS03420	Aas03420 DNA encod	C 314	13.8	76.7	702	2	AAQ25195	Aaq25195 Human pro	
C 242	13.8	76.7	325	5	AAF68351	Aaf68351 Human lun	C 315	13.8	76.7	711	3	AAF12025	Aaf12025 Aspergill	
C 243	13.8	76.7	326	6	ABK38262	Abk38262 cDNA enco	C 316	13.8	76.7	717	10	ABD53471	Abd53471 Primary r	
C 244	13.8	76.7	327	6	ACA10591	Aca10591 Human lun	C 317	13.8	76.7	729	11	ABD06440	Abd06440 Pseudomon	
C 245	13.8	76.7	328	8	ABX99542	Abx99542 Lung canc	C 318	13.8	76.7	748	12	ADP20342	Adp20342 Eucalyptu	
C 246	13.8	76.7	329	10	ADH45788	Adh45788 Human lun	C 319	13.8	76.7	752	5	AAH294247	Aah294247 Human foe	
C 247	13.8	76.7	330	12	ADP73235	Adp73235 Human lun	C 320	13.8	76.7	763	12	ADO39601	Ado39601 Yeast RNA	
C 248	13.8	76.7	331	3	AAZ58211	Aaz58211 Corn phos	C 321	13.8	76.7	770	4	AAK83703	Aak83703 Human imm	
C 249	13.8	76.7	332	10	ABX93279	Abx93279 Corn EST	C 322	13.8	76.7	774	11	ABD06565	Abd06565 Pseudomon	
C 250	13.8	76.7	333	4	AAK62911	Aak62911 Human imm	C 323	13.8	76.7	793	11	ADM45608	Adm45608 Insect re	
C 251	13.8	76.7	334	5	AAS34548	Aas34548 Human DNA	C 324	13.8	76.7	815	2	AAV04163	Aav04163 Phycophth	
C 252	13.8	76.7	335	5	AAS34547	Aas34547 Human DNA	C 325	13.8	76.7	822	2	AAV04164	Aav04164 Phycophth	
C 253	13.8	76.7	336	5	AAF67030	Aaf67030 Novel hum	C 326	13.8	76.7	840	11	ADM02788	Adm02788 Human CDN	
C 254	13.8	76.7	337	5	AAS33556	Aas33556 Human CDN	C 327	13.8	76.7	851	5	AAS92113	Aas92113 DNA encod	
C 255	13.8	76.7	338	6	ABK79643	Abk79643 Bacillus	C 328	13.8	76.7	852	8	ACA36612	Aca36612 Prokaryot	
C 256	13.8	76.7	339	402	ABK79643	Abk79643 Bacillus	C 329	13.8	76.7	853	10	ADB58007	Adb58007 Toxicity-	
C 257	13.8	76.7	340	3	AAH30392	Aah30392 Human col	C 330	13.8	76.7	853	10	ADB58007	Adb58007 Toxicity-	
C 258	13.8	76.7	341	5	AAF67045	Aaf67045 Novel hum	C 331	13.8	76.7	859	12	ADO15770	Ado15770 4 synthet	
C 259	13.8	76.7	342	5	ABAI2949	Abai2949 Human ner	C 332	13.8	76.7	861	6	AAZ34586	Aaz34586 Chlamydia	
C 260	13.8	76.7	343	5	ADI68150	Adi68150 Human ova	C 333	13.8	76.7	866	6	ABK89022	Abk89022 Human S20	
C 261	13.8	76.7	344	5	ADI74521	Adi74521 Human ova	C 334	13.8	76.7	867	10	ADG32855	Adg32855 Human DNA	
C 262	13.8	76.7	345	5	ABV18197	Abv18197 Human pro	C 335	13.8	76.7	906	3	AAK80565	Aak80565 Human sec	
C 263	13.8	76.7	346	5	ACH23777	Ach23777 Human adu	C 336	13.8	76.7	913	2	AAQ99790	Aaq99790 Plant SAR	
C 264	13.8	76.7	347	448	ACH23777	Ach23777 Human pro	C 337	13.8	76.7	923	6	ABQ54238	Abq54238 Human ova	
C 265	13.8	76.7	348	4	AAF63541	Aaf63541 Mushroom	C 338	13.8	76.7	937	6	ABK92408	Abk92408 Human pro	
C 266	13.8	76.7	349	4	AAI15295	Aai15295 Probe #52	C 339	13.8	76.7	940	5	ABV29628	Abv29628 Human pro	
C 267	13.8	76.7	350	4	ABAS3766	Abas3766 Human foe	C 340	13.8	76.7	942	4	AAI58870	Aai58870 Human pol	
C 268	13.8	76.7	351	4	AAI33395	Aai33395 Probe #20	C 341	13.8	76.7	942	5	ADQ99092	Adq99092 DNA encod	
C 269	13.8	76.7	352	4	ABA43323	Ab43323 Human bre	C 342	13.8	76.7	942	5	ADB48852	Adb48852 Novel hum	
C 270	13.8	76.7	353	4	ABA23513	Aba23513 Probe #19	C 343	13.8	76.7	948	3	AAK42910	Aak42910 Arabidops	
C 271	13.8	76.7	354	4	AAK27483	Aak27483 Human bon	C 344	13.8	76.7	978	3	AAK42910	Aak42910 Arabidops	
C 272	13.8	76.7	355	4	AAK20208	Aak20208 Human bra	C 345	13.8	76.7	987	3	AAK43132	Aak43132 Arabidops	
C 273	13.8	76.7	356	4	ABSI1983	Abi1983 Probe #19	C 346	13.8	76.7	987	12	ADJ44392	Adj44392 Plant CDN	
C 274	13.8	76.7	357	4	ABSI1969	Abi1969 Human gen	C 347	13.8	76.7	1008	4	AAI60656	Aai60656 Human pol	
C 275	13.8	76.7	358	6	ACH24465	Ach24465 Human foe	C 348	13.8	76.7	1017	4	AAD20823	Aad20823 Human CHR	
C 276	13.8	76.7	359	4	AAF63541	Aaf63541 Mushroom	C 349	13.8	76.7	1035	9	ADA31244	Ada31244 DNA encod	
C 277	13.8	76.7	360	4	AAI15295	Aai15295 Probe #52	C 350	13.8	76.7	1038	10	ADC92536	Adc92536 E. faeciu	
C 278	13.8	76.7	361	4	ABAS3766	Abas3766 Human foe	C 351	13.8	76.7	1056	5	ADL45676	Adl45676 Human ova	
C 279	13.8	76.7	362	5	AAI39792	Aai39792 Human ova	C 352	13.8	76.7	1101	3	AAK50184	Aak50184 Arabidops	
C 280	13.8	76.7	363	3	AAQ00700	Aaq00700 Human sec	C 353	13.8	76.7	1142	2	AAI13351	Aai13351 Enterococ	
C 281	13.8	76.7	364	12	ADJ10698	Adj10698 Recombina	C 354	13.8	76.7	1142	6	ABS99146	Abs99146 Enterococ	
C 282	13.8	76.7	365	491	ADJ10993	Adj10993 Recombina	C 355	13.8	76.7	1149	12	ADI16399	Adi16399 Human pro	
C 283	13.8	76.7	366	3	ACH3895	Ach3895 Human sec	C 356	13.8	76.7	1157	5	ASB88036	Asb88036 DNA encod	
C 284	13.8	76.7	367	3	ACH35914	Ach35914 Human end	C 357	13.8	76.7	1257	10	ABX06609	Abx06609 S. pneumo	
C 285	13.8	76.7	368	500	ACH35914	Ach35914 Human ORF	C 358	13.8	76.7	1290	8	ACA33540	Aca33540 Prokaryot	
C 286	13.8	76.7	369	5	ABN17008	Abn17008 Human ORF	C 359	13.8	76.7	1293	8	ACA33540	Aca33540 Prokaryot	
C 287	13.8	76.7	370	510	ADI74555	Adi74555 Human ova	C 360	13.8	76.7	1347	12	ADM35744	Adm35744 Novel hum	
C 288	13.8	76.7	371	5	ADI68184	Adi68184 Human ova	C 361	13.8	76.7	1370	9	ACC48574	Acc48574 Mouse TMD	
C 289	13.8	76.7	372	533	ADBS1318	Adbs1318 Primary r	C 362	13.8	76.7	1389	3	AAZ58192	Aaz58192 Corn phos	
C 290	13.8	76.7	373	4	AAS52243	Aas52243 Staphyloc	C 363	13.8	76.7	1389	10	ABX93260	Abx93260 EST encod	
C 291	13.8	76.7	374	4	AAI18366	Aai18366 Probe #82	C 364	13.8	76.7	1440	12	ADJ44554	Adj44554 Plant CDN	
C 292	13.8	76.7	375	4	ABA63369	Ab63369 Human foe	C 365	13.8	76.7	1449	4	AAI16755	Aai16755 Human nov	
C 293	13.8	76.7	376	4	AAI43481	Aai43481 Probe #12	C 366	13.8	76.7	1449	10	ADC22047	Adc22047 Human CDN	
C 294	13.8	76.7	377	4	ABA30572	Ab30572 Probe #90	C 367	13.8	76.7	1451	3	AAF21739	Aaf21739 Human bre	
C 295	13.8	76.7	378	4	AAK37611	Aak37611 Human bon	C 368	13.8	76.7	1455	6	AAI18563	Aai18563 Xylella f	
C 296	13.8	76.7	379	4	AAK11906	Aak11906 Human bra	C 369	13.8	76.7	1472	4	ABL14765	Abi14765 Drosophil	
C 297	13.8	76.7	380	4	ABK37264	Abk37264 Human liv	C 370	13.8	76.7	1473	8	ACA31126	Aca31126 Prokaryot	
C 298	13.8	76.7	381	552	ABSI1596	Abi1596 Human gen	C 371	13.8	76.7	1482	10	ADG43047	Adg43047 Microbe D	
C 299	13.8	76.7	382	9	ACL24927	Acl24927 DNA clone	C 372	13.8	76.7	1482	12	ADH61806	Adh61806 Spingobio	
C 300	13.8	76.7	383	4	AAI04977	Aai04977 Human rep	C 373	13.8	76.7	1500	6	ABN69867	Abn69867 Streptoco	
C 301	13.8	76.7	384	4	ABL97870	Abi97870 Human tes	C 374	13.8	76.7	1531	6	ASB67787	Asb67787 Human rec	
C 302	13.8	76.7	385	6	ABQ55383	Abq55383 Human ova	C 375	13.8	76.7	1602	6	ABN69566	Abn69566 Streptoco	
C 303	13.8	76.7	386	11	ABD06537	Abd06537 Pseudomon	C 376	13.8	76.7	1605	8	ACA50690	Aca50690 Prokaryot	
C 304	13.8	76.7	387	10	ADC08866	Adc08866 Corn DNA	C 377	13.8	76.7	1638	4	AAI71129	Aai71129 C. glutam	
C 305	13.8	76.7	388	12	ADJ44662	Adj44662 Plant CDN	C 378	13.8	76.7	1698	4	AAI07467	Aai07467 Human rep	
C 306	13.8	76.7	389	3	AAK43125	Aak43125 Arabidops	C 379	13.8	76.7	1733	4	AAI07467	Aai07467 Human rep	
C 307	13.8	76.7	390	9	AAH32356	Aah32356 Human olf	C 380	13.8	76.7	1733	10	ADC22062	Adc22062 Human CDN	
C 308	13.8	76.7	391	645	AAH32356	Aah32356 Human olf	C 381	13.8	76.7	1822	5	AAH84352	Aah84352 DNA encod	
C 309	13.8	76.7	392	652	ABZ73225	Abz73225 Rice leaf	C 382	13.8	76.7	1840	5	ADL62056	Adl62056 Human ova	
C 310	13.8	76.7	393	667	10	ABX99148	Abx99148 Rice endo	C 383	13.8	76.7	1857	5	AAH66773	Aah66773 C. glutami
C 311	13.8	76.7	394	669	11	ABD06510	Abd06510 Pseudomon	C 384	13.8	76.7	1857	10	ADJ87436	Adj87436 DNA repli
C 312	13.8	76.7	395	683	3	AAF12807	Aaf12807 Aspergill	C 385	13.8	76.7	1943	4	ADL4085	Adl4085 Drosophil
C 313	13.8	76.7	396	698	10	ADK57711	Adk57711 Plant DNA	C 386	13.8	76.7	2000	8	ADA71875	Ada71875 Rice Gene

C 387	13.8	76.7	2000	8	ADA72346	Ada72346 Rice gene	460	13.8	76.7	4796	5	ABA18580	Abal8580 Human ner
C 388	13.8	76.7	2000	12	ADJ11210	Adj11210 Plant cDN	461	13.8	76.7	4796	9	ADB60896	Adb60896 Connectiv
C 389	13.8	76.7	2030	2	AAV29218	AAV29218 Nucleotid	C 462	13.8	76.7	5702	4	ABL03538	Ab103538 Drosophil
C 390	13.8	76.7	2030	6	ABK63800	Abk63800 Rat sequ	C 462	13.8	76.7	5702	4	ABL03538	Ab103538 Drosophil
C 391	13.8	76.7	2098	10	ADB58468	ADB58468 Toxicity	464	13.8	76.7	6111	3	AA92472	Aa92472 Shewanell
C 392	13.8	76.7	2098	10	ADB53055	ADB53055 Primary r	465	13.8	76.7	6111	3	AA92472	Aa92472 Shewanell
C 393	13.8	76.7	2098	10	ABT42098	Abt42098 Toxicity	466	13.8	76.7	6149	4	AAK90926	Aak90926 Human dig
C 394	13.8	76.7	2098	12	ADP72824	Adp72824 Renal tox	467	13.8	76.7	6149	5	AAK90926	Aak90926 Human dig
C 395	13.8	76.7	2133	4	AAH11475	Aah11475 Human cDN	468	13.8	76.7	6149	5	AAK90926	Aak90926 Human dig
C 396	13.8	76.7	2145	4	ABL29181	Ab129181 Drosophil	469	13.8	76.7	6149	6	ABN90315	Abn90315 Human liv
C 397	13.8	76.7	2179	8	ACC46730	Acc46730 Human dit	470	13.8	76.7	6149	6	ABN90315	Abn90315 Human liv
C 398	13.8	76.7	2226	10	ADE55348	Ades55348 Rat gene	C 471	13.8	76.7	6149	11	ADJ15228	Adj15228 Human liv
C 399	13.8	76.7	2234	4	ABL24922	Ab124922 Drosophil	C 472	13.8	76.7	6159	4	AAK75604	Aak75604 Human imm
C 400	13.8	76.7	2251	2	AAV11153	Aav11153 Mouse XRC	C 473	13.8	76.7	6164	4	AAK75604	Aak75604 Human imm
C 401	13.8	76.7	2254	4	AAH33183	Aah33183 Human col	C 474	13.8	76.7	6164	4	AAK75604	Aak75604 Human imm
C 402	13.8	76.7	2259	3	AAAG61279	Aaag61279 Human sec	C 475	13.8	76.7	6167	4	AAK75609	Aak75609 Human imm
C 403	13.8	76.7	2311	6	ABQ77787	Abq77787 Human ATP	C 476	13.8	76.7	6224	12	ADQ39654	Adq39654 Yeast RNA
C 404	13.8	76.7	2346	3	AAA95821	Aaa95821 Human met	C 477	13.8	76.7	6224	12	ADQ39654	Adq39654 Yeast RNA
C 405	13.8	76.7	2360	6	ABQ69091	Abq69091 Listeria	C 478	13.8	76.7	6224	12	ADQ39654	Adq39654 Yeast RNA
C 406	13.8	76.7	2361	8	ACA48407	Acca48407 Prokaryot	479	13.8	76.7	6224	12	ADQ39654	Adq39654 Yeast RNA
C 407	13.8	76.7	2448	6	ABN79854	Abn79854 Fungal ZB	C 480	13.8	76.7	7568	5	AAK87784	Aak87784 DNA encod
C 408	13.8	76.7	2515	2	AAV11152	Aav11152 Mouse XRC	C 481	13.8	76.7	7568	5	AAK87784	Aak87784 DNA encod
C 409	13.8	76.7	2633	4	AAK65400	Aak65400 Human imm	C 482	13.8	76.7	7568	12	ADQ19384	Adq19384 Marker ge
C 410	13.8	76.7	2643	10	ADF28104	Adf28104 Adiponect	C 483	13.8	76.7	7572	10	ABX74469	Abx74469 Human cDN
C 411	13.8	76.7	2670	4	AAH20226	Aah20226 Human ADA	C 484	13.8	76.7	7580	12	ADQ23621	Adq23621 Human sof
C 412	13.8	76.7	2670	5	AAH20226	Aah20226 Human ADA	C 485	13.8	76.7	7580	12	ADQ23621	Adq23621 Human sof
C 413	13.8	76.7	2670	5	AAH20226	Aah20226 Human ADA	C 486	13.8	76.7	7580	12	ADQ23621	Adq23621 Human sof
C 414	13.8	76.7	2730	10	ADJ92166	Adj92166 Human hai	C 487	13.8	76.7	7754	12	ADI67008	Adi67008 Novel Lac
C 415	13.8	76.7	2779	11	ADMO1459	Adm01459 Human cDN	C 488	13.8	76.7	7754	12	ADI67008	Adi67008 Novel Lac
C 416	13.8	76.7	2790	6	ABZ12893	Abz12893 Arabidops	C 489	13.8	76.7	9324	4	AAK75610	Aak75610 Human imm
C 417	13.8	76.7	2790	8	ABZ42029	Abz42029 Arabidops	C 490	13.8	76.7	9324	4	AAK75610	Aak75610 Human imm
C 418	13.8	76.7	2790	8	ADA68555	Ada68555 Arabidops	C 491	13.8	76.7	9324	4	AAK75610	Aak75610 Human imm
C 419	13.8	76.7	2901	4	ABSL17332	Ab117332 Drosophil	C 492	13.8	76.7	10434	10	ADE48682	Ade48682 Human car
C 420	13.8	76.7	2913	4	AAK51467	Aak51467 Human pol	C 493	13.8	76.7	10434	10	ADE48682	Ade48682 Human car
C 421	13.8	76.7	2913	10	ADP28755	Adp28755 Arabidops	C 494	13.8	76.7	10434	10	ADE48682	Ade48682 Human car
C 422	13.8	76.7	3008	2	AAZ32001	Aaz32001 Human MET	495	13.8	76.7	10519	4	ABK42741	Abk42741 Genomic s
C 423	13.8	76.7	3008	5	AAK90058	Aak90058 Human MET	496	13.8	76.7	10519	5	ABK42741	Abk42741 Genomic s
C 424	13.8	76.7	3037	6	ABK48733	Abk48733 DNA encod	497	13.8	76.7	10519	5	ABK42741	Abk42741 Genomic s
C 425	13.8	76.7	3037	10	ACF04932	Acf04932 Plant wit	C 498	13.8	76.7	10519	5	ABK42741	Abk42741 Genomic s
C 426	13.8	76.7	3037	12	ADP90957	Adp90957 Figleaf g	C 499	13.8	76.7	10519	5	ABK42741	Abk42741 Genomic s
C 427	13.8	76.7	3078	5	AAV05045	Aav05045 A NADPH o	C 500	13.8	76.7	10519	5	ABK42741	Abk42741 Genomic s
C 428	13.8	76.7	3078	5	AAV05045	Aav05045 A NADPH o	C 501	13.8	76.7	10519	5	ABK42741	Abk42741 Genomic s
C 429	13.8	76.7	3078	5	AAV05045	Aav05045 A NADPH o	C 502	13.8	76.7	10519	5	ABK42741	Abk42741 Genomic s
C 430	13.8	76.7	3088	12	ADK65991	Adk65991 Arabidops	503	13.8	76.7	11283	4	AAK82965	Aak82965 Human imm
C 431	13.8	76.7	3126	6	ABN86300	Abn86300 Human pro	504	13.8	76.7	11283	4	AAK82965	Aak82965 Human imm
C 432	13.8	76.7	3165	8	ACA33650	Acca33650 Prokaryot	505	13.8	76.7	11283	4	AAK82965	Aak82965 Human imm
C 433	13.8	76.7	3168	8	ACA33445	Acca33445 Prokaryot	506	13.8	76.7	11283	4	AAK82965	Aak82965 Human imm
C 434	13.8	76.7	3172	4	AAK85276	Aak85276 Human imm	507	13.8	76.7	11283	4	AAK82965	Aak82965 Human imm
C 435	13.8	76.7	3172	4	AAK85276	Aak85276 Human imm	508	13.8	76.7	11283	4	AAK82965	Aak82965 Human imm
C 436	13.8	76.7	3172	4	AAK85276	Aak85276 Human imm	509	13.8	76.7	11283	4	AAK82965	Aak82965 Human imm
C 437	13.8	76.7	3213	10	ADC33454	Adc33454 E. faeciu	C 510	13.8	76.7	13255	4	ABL27900	Ab127900 Drosophil
C 438	13.8	76.7	3227	12	ADK70389	Adk70389 Respiraco	C 511	13.8	76.7	13255	4	ABL27900	Ab127900 Drosophil
C 439	13.8	76.7	3376	11	ADMO2979	Adm02979 Human cDN	C 512	13.8	76.7	13255	4	ABL27900	Ab127900 Drosophil
C 440	13.8	76.7	3376	11	ADMO2979	Adm02979 Human cDN	C 513	13.8	76.7	13255	4	ABL27900	Ab127900 Drosophil
C 441	13.8	76.7	3638	4	AAK63441	Aak63441 Murine AD	C 514	13.8	76.7	13255	4	ABL27900	Ab127900 Drosophil
C 442	13.8	76.7	3669	4	AAK07466	Aak07466 Human rep	C 515	13.8	76.7	13255	4	ABL27900	Ab127900 Drosophil
C 443	13.8	76.7	3711	10	ADK65991	Adk65991 Arabidops	C 516	13.8	76.7	13255	4	ABL27900	Ab127900 Drosophil
C 444	13.8	76.7	3771	12	ADK65991	Adk65991 Arabidops	C 517	13.8	76.7	13255	4	ABL27900	Ab127900 Drosophil
C 445	13.8	76.7	3818	4	ABL22970	Ab122970 Drosophil	C 518	13.8	76.7	13255	4	ABL27900	Ab127900 Drosophil
C 446	13.8	76.7	3950	10	ADK65991	Adk65991 Arabidops	C 519	13.8	76.7	13255	4	ABL27900	Ab127900 Drosophil
C 447	13.8	76.7	4019	4	ABL13312	Ab113312 Drosophil	C 520	13.8	76.7	13255	4	ABL27900	Ab127900 Drosophil
C 448	13.8	76.7	4025	4	ABL14764	Ab114764 Drosophil	521	13.8	76.7	13255	4	ABL27900	Ab127900 Drosophil
C 449	13.8	76.7	4033	4	AAI61062	Aai61062 Human pol	522	13.8	76.7	13255	4	ABL27900	Ab127900 Drosophil
C 450	13.8	76.7	4033	4	AAI61062	Aai61062 Human pol	C 523	13.8	76.7	13255	4	ABL27900	Ab127900 Drosophil
C 451	13.8	76.7	4091	10	ADB33025	Adb33025 Aspergill	524	13.8	76.7	13255	4	ABL27900	Ab127900 Drosophil
C 452	13.8	76.7	4280	4	AAK07469	Aak07469 Human rep	525	13.8	76.7	13255	4	ABL27900	Ab127900 Drosophil
C 453	13.8	76.7	4554	10	ADB33027	Adb33027 Aspergill	526	13.8	76.7	13255	4	ABL27900	Ab127900 Drosophil
C 454	13.8	76.7	4605	10	ADB33027	Adb33027 Aspergill	C 527	13.8	76.7	13255	4	ABL27900	Ab127900 Drosophil
C 455	13.8	76.7	4605	10	ADB33027	Adb33027 Aspergill	528	13.8	76.7	13255	4	ABL27900	Ab127900 Drosophil
C 456	13.8	76.7	4638	4	ABL29180	Ab129180 Drosophil	529	13.8	76.7	13255	4	ABL27900	Ab127900 Drosophil
C 457	13.8	76.7	4657	12	ADN05287	Adn05287 Antipsosi	530	13.8	76.7	13255	4	ABL27900	Ab127900 Drosophil
C 458	13.8	76.7	4710	4	ABK42740	Abk42740 Genomic s	531	13.8	76.7	13255	4	ABL27900	Ab127900 Drosophil
C 459	13.8	76.7	4796	4	ABK42740	Abk42740 Genomic s	C 532	13.8	76.7	13255	4	ABL27900	Ab127900 Drosophil

C 533	13.8	76.7	32167	4	AAL05509	Human rep	606	13.8	76.7	183999	4	AAF92831	Human ABC
C 534	13.8	76.7	33769	5	ABA92622	Human HBM	607	13.8	76.7	188971	12	ADL08108	Human gen
C 535	13.8	76.7	33769	6	ABK232781	Human big	608	13.8	76.7	243428	12	ADF51132	Human P-R
C 536	13.8	76.7	33769	8	ACC45363	Human HBM	609	13.8	76.7	249487	6	ABN85733	Mouse gen
C 537	13.8	76.7	33769	10	ADB98063	HBM-relat	610	13.8	76.7	259202	12	ADQ18492	Human sof
C 538	13.8	76.7	33769	10	ADB98063	HBM-relat	611	13.8	76.7	262029	6	ABS56564	Human SUL
C 539	13.8	76.7	34886	12	ADQ344335_6	Continuation (7 of	612	13.8	76.7	262029	10	ADN16204	Human sul
C 540	13.8	76.7	34917	4	AAK70686	Human imm	613	13.8	76.7	349881	10	ACC86642	Human GPC
C 541	13.8	76.7	39353	4	AAK67232	Human imm	614	13.8	76.7	349881	5	AAH68529	C glutami
C 542	13.8	76.7	39353	4	AAK65396	Human imm	615	13.6	75.6	21	21	AAV67377	Nucleotid
C 543	13.8	76.7	39358	4	AAK65397	Human imm	616	13.6	75.6	227	2	AAK10748	Human bia
C 544	13.8	76.7	39358	4	AAK65723	Human imm	617	13.4	74.4	230	12	ADP09447	PCR prime
C 545	13.8	76.7	39801	6	ABK93462	Human CDN	618	13.4	74.4	158	2	AAK51908	Human sec
C 546	13.8	76.7	40138	2	AAV81946	AAV1520 V. marinu	619	13.4	74.4	203	3	AAK08177	Human sec
C 547	13.8	76.7	40138	3	AAA71520	AAV1520 V. marinu	620	13.4	74.4	230	3	AAK29970	Human sec
C 548	13.8	76.7	41400	10	ABK77189	Mouse GPC	621	13.4	74.4	288	6	ABL72680	Corri cass
C 549	13.8	76.7	43419	10	ADCB6998	Human GPC	622	13.4	74.4	288	6	ABX37056	Bovine ES
C 550	13.8	76.7	50000	6	ADA43380	Human ast	623	13.4	74.4	291	4	AAK15061	Human bre
C 551	13.8	76.7	50000	6	ABA98944	Human ast	624	13.4	74.4	293	4	AAK23914	Human bre
C 552	13.8	76.7	52302	9	ADA02738	Human CCN	625	13.4	74.4	301	4	AAK12171	Human bra
C 553	13.8	76.7	52302	10	ADB72476	Human CCN	626	13.4	74.4	310	2	AAK59845	Human bra
C 554	13.8	76.7	52302	10	ADC85218	Human CCN	627	13.4	74.4	315	4	AAK21054	Human bra
C 555	13.8	76.7	52302	12	ADM74333	Human car	628	13.4	74.4	326	3	AAK00621	Human sec
C 556	13.8	76.7	55827	8	ACA60949	DNA encod	629	13.4	74.4	327	2	AAK40630	Human sec
C 557	13.8	76.7	55827	10	ABX13671	Human pro	630	13.4	74.4	357	2	AAQ61279	Human bra
C 558	13.8	76.7	63000	6	ABS67634	Human cas	631	13.4	74.4	362	5	AAF65636	Novel hum
C 559	13.8	76.7	72928	2	AAZ18355	Human AST	632	13.4	74.4	373	4	AAI89609	Human pol
C 560	13.8	76.7	72928	3	AAA80253	Human AST	633	13.4	74.4	375	5	AAF67151	Novel hum
C 561	13.8	76.7	87761	11	ADL27164	Human gen	634	13.4	74.4	402	10	ACF67497	Photornab
C 562	13.8	76.7	88624	9	ADL62889	Human alp	635	13.4	74.4	413	5	ABV07586	Human nov
C 563	13.8	76.7	94529	9	ADA03086	Human hCG	636	13.4	74.4	420	8	ABX05238	Human nov
C 564	13.8	76.7	94529	9	ADA66370	Human hCG	637	13.4	74.4	424	9	ACH17031	Human adu
C 565	13.8	76.7											

c 679	13.4	74.4	1298	12	AD080750
c 680	13.4	74.4	1347	3	AAV19864 Gallus
c 681	13.4	74.4	1392	3	AAAG4188 Gallus
c 682	13.4	74.4	1392	3	AAAG59709 Human sec
c 683	13.4	74.4	1399	5	AAH68578 Human
c 684	13.4	74.4	1418	12	ADP07701 Human
c 685	13.4	74.4	1466	3	AAA64189 Nucleotid
c 686	13.4	74.4	1560	8	ADAG9759 Rice gene
c 687	13.4	74.4	1560	12	ADJ35951 Plant cDN
c 688	13.4	74.4	1587	2	AAV19863 Gallus
c 689	13.4	74.4	1707	10	AD048056 Rat gene
c 690	13.4	74.4	1707	10	AD048053 Rat gene
c 691	13.4	74.4	1713	4	AAI59955 Human pol
c 692	13.4	74.4	1723	4	AAAF4271 Maize cal
c 693	13.4	74.4	1754	6	AAI198973 Human can
c 694	13.4	74.4	1755	1	AAAG0294 C-termina
c 695	13.4	74.4	1758	5	AAAS77347 DNA enco
c 696	13.4	74.4	1758	5	AAAS74884 DNA enco
c 697	13.4	74.4	1765	6	ABK33552 cDNA enco
c 698	13.4	74.4	1768	8	ACA86533 Novel hum
c 699	13.4	74.4	1768	9	ABT44242 Human PRO
c 700	13.4	74.4	1768	9	ABT44525 Human PRO
c 701	13.4	74.4	1768	9	ABT44525 Human PRO
c 702	13.4	74.4	1768	9	ABT43898 Human mem
c 703	13.4	74.4	1768	9	ADB83523 Novel hum
c 704	13.4	74.4	1768	9	ADB80629 Novel hum
c 705	13.4	74.4	1768	9	ADB73170 Novel hum
c 706	13.4	74.4	1768	9	ADB78252 Novel hum
c 707	13.4	74.4	1768	10	ADB84900 Human PRO
c 708	13.4	74.4	1768	10	ADB78006 Novel hum
c 709	13.4	74.4	1768	10	ADB87072 Human PRO
c 710	13.4	74.4	1768	10	ADB84654 Human PRO
c 711	13.4	74.4	1768	10	ADB83769 Novel hum
c 712	13.4	74.4	1768	10	ADB72924 Novel hum
c 713	13.4	74.4	1768	10	ADCB6762 Human PRO
c 714	13.4	74.4	1768	10	ADCB1752 Human PRO
c 715	13.4	74.4	1768	10	ADCA9783 Novel hum
c 716	13.4	74.4	1768	10	ADCA48982 Novel hum
c 717	13.4	74.4	1768	10	ADCA9499 Novel hum
c 718	13.4	74.4	1768	10	ADCA47360 Novel hum
c 719	13.4	74.4	1768	10	ADCA47105 Novel hum
c 720	13.4	74.4	1768	10	ADCB77980 Novel hum
c 721	13.4	74.4	1768	10	ADCB66215 Novel hum
c 722	13.4	74.4	1768	10	ADCB77734 Novel hum
c 723	13.4	74.4	1768	10	ADCB50697 Novel hum
c 724	13.4	74.4	1768	10	ADCB50943 Novel hum
c 725	13.4	74.4	1768	10	ADCB50424 Human PRO
c 726	13.4	74.4	1768	10	ADCB50178 Human PRO
c 727	13.4	74.4	1768	10	ADCB51189 Novel hum
c 728	13.4	74.4	1768	10	ACAB66857 cDNA enco
c 729	13.4	74.4	1768	12	ADCB68039 Novel hum
c 730	13.4	74.4	1768	12	ADCB48736 Novel hum
c 731	13.4	74.4	1768	12	ADCB20907 Novel hum
c 732	13.4	74.4	1768	12	ADCB50751 Human PRO
c 733	13.4	74.4	1768	12	ADCB74580 Human PRO
c 734	13.4	74.4	1768	12	ADCB75726 Novel hum
c 735	13.4	74.4	1768	12	ADCB4958 Novel hum
c 736	13.4	74.4	1768	12	ADCB6784 Novel hum
c 737	13.4	74.4	1768	12	ADCB20661 Novel hum
c 738	13.4	74.4	1768	12	ADCB38958 Novel hum
c 739	13.4	74.4	1768	12	ADCB50505 Human PRO
c 740	13.4	74.4	1768	12	ADCB73490 Human PRO
c 741	13.4	74.4	1768	12	ADCB78330 Novel hum
c 742	13.4	74.4	1768	12	ADCB21153 Novel hum
c 743	13.4	74.4	1768	12	ADCB77268 Novel hum
c 744	13.4	74.4	1768	12	ADCB20415 Novel hum
c 745	13.4	74.4	1768	12	ADCB75480 Human PRO
c 746	13.4	74.4	1768	12	ADCB73996 Human PRO
c 747	13.4	74.4	1768	12	ADCB74242 Human PRO
c 748	13.4	74.4	1768	12	ADCB75972 Novel hum
c 749	13.4	74.4	1768	12	ADCB85464 Novel hum
c 750	13.4	74.4	1768	12	ADCB50513 Human PRO
c 751	13.4	74.4	1768	12	ADCB75226 Human PRO

752	13.4	74.4	1976	12	ADD76770	Novel hum
753	13.4	74.4	1976	12	AD86538	Novel hum
754	13.4	74.4	1976	12	ADD78006	Novel hum
755	13.4	74.4	1976	12	ADD77514	Novel hum
756	13.4	74.4	1976	12	ADD77760	Novel hum
757	13.4	74.4	1976	12	AD85218	Novel hum
758	13.4	74.4	1976	12	ADD73750	Human PRO
759	13.4	74.4	1976	12	ADD74488	Human PRO
760	13.4	74.4	1976	12	ADD77016	Novel hum
761	13.4	74.4	1976	12	AD85710	Novel hum
762	13.4	74.4	1976	12	AD85710	Novel hum
763	13.4	74.4	1976	12	AD85710	Novel hum
764	13.4	74.4	1976	12	AD85710	Novel hum
765	13.4	74.4	1976	12	AD85710	Novel hum
766	13.4	74.4	1976	12	AD85710	Novel hum
767	13.4	74.4	1976	12	AD85710	Novel hum
768	13.4	74.4	1976	12	AD85710	Novel hum
769	13.4	74.4	1976	12	AD85710	Novel hum
770	13.4	74.4	1976	12	AD85710	Novel hum
771	13.4	74.4	1976	12	AD85710	Novel hum
772	13.4	74.4	1976	12	AD85710	Novel hum
773	13.4	74.4	1976	12	AD85710	Novel hum
774	13.4	74.4	1976	12	AD85710	Novel hum
775	13.4	74.4	1976	12	AD85710	Novel hum
776	13.4	74.4	1976	12	AD85710	Novel hum
777	13.4	74.4	2000	10	ACC60625	Gene sequ
778	13.4	74.4	2000	10	ADK62927	Disease t
779	13.4	74.4	2015	5	AA863758	DNA encod
780	13.4	74.4	2016	1	AAN60292	Intron fr
781	13.4	74.4	2054	3	AZ43779	Human fet
782	13.4	74.4	2086	5	ABA09714	Human bon
783	13.4	74.4	2143	10	AD63766	Human tdr
784	13.4	74.4	2164	12	ADL61106	Human tdr
785	13.4	74.4	2172	12	AD181551	Rat epith
786	13.4	74.4	2172	12	AD181555	Rat calci
787	13.4	74.4	2190	6	ABA93118	Abasid
788	13.4	74.4	2190	6	AAU41890	Abasid
789	13.4	74.4	2190	6	AAU41890	Abasid
790	13.4	74.4	2226	3	AAV12945	DNA encod
791	13.4	74.4	2233	2	AAV12945	DNA encod
792	13.4	74.4	2279	4	ABU18046	Drosoph
793	13.4	74.4	2290	1	AAN60293	Chromsom
794	13.4	74.4	2334	5	AA574520	DNA encod
795	13.4	74.4	2334	5	AA577522	DNA encod
796	13.4	74.4	2400	4	ABU28592	Drosoph
797	13.4	74.4	2458	12	ADQ13599	Tomato et
798	13.4	74.4	2479	3	AA295382	Tobacco e
799	13.4	74.4	2509	12	ADQ13600	Tomato et
800	13.4	74.4	2517	4	ABU23130	Drosoph
801	13.4	74.4	2528	11	ADMO2164	Human cDN
802	13.4	74.4	2570	10	AD86814	Petunia P
803	13.4	74.4	2671	4	ABU03242	Drosoph
804	13.4	74.4	2709	8	ACA39601	Prokaryot
805	13.4	74.4	2715	5	ADQ13613	Drosoph
806	13.4	74.4	2739	4	ABU10384	Drosoph
807	13.4	74.4	2745	11	ADMO1755	Human cDN
808	13.4	74.4	2749	6	ABK35261	Human cDN
809	13.4	74.4	2852	4	ABU10572	Drosoph
810	13.4	74.4	2905	4	AA158169	Human pol
811	13.4	74.4	2905	5	ADQ98375	DNA encod
812	13.4	74.4	2905	9	ADQ98375	DNA encod
813	13.4	74.4	2910	6	ABZ32182	Candida a
814	13.4	74.4	2928	10	ADBS2709	Primary r
815	13.4	74.4	2928	12	ADP72774	Renal Cox
816	13.4	74.4	3057	4	AAK81647	Human imm
817	13.4	74.4	3057	4	AAK81648	Human imm
818	13.4	74.4	3119	2	AAK07429	Human sapi
819	13.4	74.4	3144	11	ADMO3175	Human cDN
820	13.4	74.4	3289	6	ABS56241	Human G p
821	13.4	74.4	3309	6	AD43312	Human DnC
822	13.4	74.4	3441	5	AA89011	DNA encod
823	13.4	74.4	3441	5	AA888675	DNA encod
824	13.4	74.4	3441	5	AA89057	DNA encod

C 825 13.4 74.4 3460 8 ACD13437 Human DNA  
C 826 13.4 74.4 3465 5 AAS72746 DNA encod  
C 827 13.4 74.4 3543 4 AAF55696 Human EPL  
C 828 13.4 74.4 3650 4 AAF55697 Human EPL  
C 829 13.4 74.4 3655 8 ACF34552 Gene enco  
C 830 13.4 74.4 3664 5 ABX71307 Human tra  
C 831 13.4 74.4 3669 6 ABE67743 Human int  
C 832 13.4 74.4 3705 3 AAS53866 Sequence  
C 833 13.4 74.4 3711 3 AAF77143 Human ORF  
C 834 13.4 74.4 3820 10 AAD59137 Human cDN  
C 835 13.4 74.4 4150 4 ABL07491 Human  
C 836 13.4 74.4 4182 10 ADB85145 Rat calci  
C 837 13.4 74.4 4298 5 ABA14784 Human ner  
C 838 13.4 74.4 4674 8 ABL13837 Drosophil  
C 839 13.4 74.4 4952 8 ABX63334 Human cDN  
C 840 13.4 74.4 5027 2 AAV19860 Gallus do  
C 841 13.4 74.4 5667 8 ABE74229 Secreted  
C 842 13.4 74.4 5667 8 ADA98758 Human sec  
C 843 13.4 74.4 5667 10 ABE67795 Human sec  
C 844 13.4 74.4 6323 4 ABL19572 Drosophil  
C 845 13.4 74.4 6623 2 AAV19051 Mitochond  
C 846 13.4 74.4 6623 2 AAV19053 Mitochond  
C 847 13.4 74.4 7364 12 ADG30623 Rice stitg  
C 848 13.4 74.4 7479 6 AAD29132 Venezuela  
C 849 13.4 74.4 7871 4 ABL13836 Drosophil  
C 850 13.4 74.4 8321 2 AAV19869 Gallus do  
C 851 13.4 74.4 8526 5 ABA18356 Human ner  
C 852 13.4 74.4 8877 4 ABL13920 Drosophil  
C 853 13.4 74.4 8877 4 AAS57138 DNA encod  
C 854 13.4 74.4 8877 10 ADC35848 Drosophil  
C 855 13.4 74.4 9014 2 AAT45836 Hepatitis  
C 856 13.4 74.4 9103 2 AAT15657 HGV-JC va  
C 857 13.4 74.4 9103 2 AAT08856 Hepatitis  
C 858 13.4 74.4 9103 2 AAV66229 Hepatitis  
C 859 13.4 74.4 9103 2 AAV56192 HGV varia  
C 860 13.4 74.4 9103 2 AAX16395 Consensus  
C 861 13.4 74.4 9103 2 AAX02467 US856134  
C 862 13.4 74.4 9103 2 AAV82137 Hepatitis  
C 863 13.4 74.4 9159 4 ABL02928 Drosophil  
C 864 13.4 74.4 9256 2 AAV23075 Fragment  
C 865 13.4 74.4 9271 2 AAV23080 Fragment  
C 866 13.4 74.4 9390 2 AAT76931 Gr230 gen  
C 867 13.4 74.4 9390 2 AAT76929 Gr230 gen  
C 868 13.4 74.4 9391 2 AAV23077 Fragment  
C 869 13.4 74.4 9391 2 AAV23076 Fragment  
C 870 13.4 74.4 9914 4 ABK42671 Genomic s  
C 871 13.4 74.4 9914 9 ADB60827 Connectiv  
C 872 13.4 74.4 10023 2 AAV52731 Human hep  
C 873 13.4 74.4 10926 4 AAK65370 Human imm  
C 874 13.4 74.4 11459 3 AAK49442 Venezuela  
C 875 13.4 74.4 12351 4 AAS41943 Genomic s  
C 876 13.4 74.4 12379 6 AAD29139 Human imm  
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C 878 13.4 74.4 12412 4 AAS41941 Genomic s  
C 879 13.4 74.4 12523 6 AAD29131 Venezuela  
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C 881 13.4 74.4 15308 4 ABL27868 Drosophil  
C 882 13.4 74.4 16518 4 AAS27832 DNA encod  
C 883 13.4 74.4 16518 4 AAK73204 Human imm  
C 884 13.4 74.4 16518 4 AAK73489 Human imm  
C 885 13.4 74.4 16518 10 ADB94635 Novel hum  
C 886 13.4 74.4 16956 3 AAZ91923 Wild type  
C 887 13.4 74.4 17736 4 ABL28554 Drosophil  
C 888 13.4 74.4 19429 4 AAS30443 DNA encod  
C 889 13.4 74.4 19429 4 AAK71692 Human imm  
C 890 13.4 74.4 19429 5 AAL06223 Human rep  
C 891 13.4 74.4 19429 5 ABA14454 Human ner  
C 892 13.4 74.4 20300 4 AAS30441 DNA encod  
C 893 13.4 74.4 20300 4 AAK71686 Human imm  
C 894 13.4 74.4 20300 4 AAL06221 Human rep  
C 895 13.4 74.4 20300 5 ABA14452 Human ner  
C 896 13.4 74.4 20453 4 ABL03244 Drosophil  
C 897 13.4 74.4 22140 4 AAS30444 DNA encod

AAK71693 Human imm  
AAL05224 Human rep  
ABA14455 Human ner  
AAS30442 DNA encod  
AAK71689 Human imm  
AAL06222 Human rep  
ABA14453 Human ner  
AAK86766 Human imm  
ABL19442 Drosophil  
ABL16558 Drosophil  
ADFI6661 Leukaemia  
ABAI7963 Human ner  
AAD26438 Human GRM  
AAD26403 Human glu  
AAD31202 Oryza sat  
ABL06102 Drosophil  
AA963664 Polymorph  
ABQ76896 Human G-P  
AD02753 Mouse Mor  
ADB72491 Mouse Mor  
ADC85233 Mouse Mor  
ADM74348 Murine ca  
ADH54712 Human VEG  
ADF62737 Cancer ba  
ADB20852 MRP1 base  
ADB7941 Human UGT  
ADB6924 Human MDR  
AD92115 Human MDR  
AAS05390 Human tit  
ABK64829 Human ben  
ADQ17315 Human sof  
ABX13540 Human RGS  
ADL13556 Osteoarth  
ADP08391 Human tit  
ABX08336 Human chr  
AD08336 Human pho  
Continuation (2 of  
Continuation (20 o  
ADL12064 Alloiococ  
ACF65383 Photothab  
ACF67367 Photothab  
ABQ84281 Chromosom  
Continuation (2 of  
ADJ25985 Human pho  
Continuation (2 of  
ADN97989 Human pho  
Continuation (2 of  
ADO50281 Human pho  
Continuation (2 of  
ADH58564 Human Na+  
ADL13728 Osteoarth  
AC02697 Human gly  
AAL02697 Human gly  
AAL92831 Human ABC  
ABT10718 Human bre  
ACF62750 Cancer ba  
ADB20869 MRP1 base  
ADB87958 Human UGT  
ADB9491 Human MDR  
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ADL13570 Osteoarth  
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ABX16034 Human Gen  
ACF62735 Cancer ba  
ACF62740 Cancer ba  
ADB20850 MRP1 base  
ADB20855 MRP1 base  
ADB87944 Human UGT  
ADB87939 Human UGT  
ADB96922 Human MDR  
ADB96927 Human MDR  
AD92113 Human MDR  
AD92116 Human MDR  
ADL13693 Osteoarth





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PI Slangenhaupt S, Gusella JF;
XX WPI; 2002-674806/72.
XX
XX New IKBKAP genes with mutations, useful for identifying a subject with
XX familial dysautonomia (FD), or for rapid carrier screening in the
XX Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or
XX prenatal diagnosis.
XX
XX Claim 1; Page; 109pp; English.
XX
XX The present invention relates to methods and compositions useful for
XX detecting mutations which cause Familial Dysautonomia (FD, Riley-Day
XX syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) [OMIM
XX 223900]. It was found that mutations in the IKBKAP gene (see ABQ80565)
XX are associated with FD. The mutation associated with the major haplotype
XX of FD, FDI mutation, is a base pair (bp) mutation, where the thymine
XX nucleotide located at bp 6 of intron 20 in the IKBKAP gene is replaced
XX with a cytosine. This results in skipping of exon 20 in the mRNA from FD
XX patients, although they continue to express varying levels of wild-type
XX message in a tissue-specific manner. The mutation associated with the
XX minor haplotype, FD2 mutation, is a bp mutation, where the guanine
XX nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a cytosine.
XX This bp mutation causes an arginine to proline missense mutation (R696P)
XX in the IKBKAP protein, which is predicted to disrupt a potential
XX phosphorylation site. The IKBKAP nucleic acid sequences are useful for
XX identifying a subject with FD and for rapid carrier screening. The IKBKAP
XX gene contains 37 exons and maps to chromosome 9q31. Note: the present
XX sequence was not shown in the specification, but was derived from the
XX human wild-type IKBKAP sequence given in Fig 6
XX
XX Sequence 66479 BP; 18271 A; 12399 C; 14128 G; 21681 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 18; DB 6; Length 66479;
XX Best Local Similarity 100.0%; Pred. NO. 33;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ATGCTTGCTACTTGGCTG 18
DB 33818 ATGCTTGCTACTTGGCTG 33801

RESULT 3
ABQ80566/c
ID ABQ80566 standard; DNA; 66479 BP.
XX
AC ABQ80566;
XX
XX 08-NOV-2002 (first entry)
XX
XX Mutant human IKBKAP gene #1.
XX
XX Human; IKBKAP; Familial Dysautonomia; FD; Riley-Day syndrome;
XX Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening;
XX FDI; mutation; gene; chromosome 9q31; ds.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX mutation replace(34201,T)
XX FT /*tag= a
XX FT mutation
XX FT replace(34201,T)
XX FT /*tag= b
XX
XX WO200259381-A2.
XX
XX 01-AUG-2002.
XX
XX 07-JAN-2002; 2002WO-US000473.
XX
XX 06-JAN-2001; 2001US-0260080P.
XX
XX (GEMO ) GEN HOSPITAL CORP.
XX

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PI Slangenhaupt S, Gusella JF;
XX WPI; 2002-674806/72.
XX
XX New IKBKAP genes with mutations, useful for identifying a subject with
XX familial dysautonomia (FD), or for rapid carrier screening in the
XX Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or
XX prenatal diagnosis.
XX
XX Claim 1; Page; 109pp; English.
XX
XX The present invention relates to methods and compositions useful for
XX detecting mutations which cause Familial Dysautonomia (FD, Riley-Day
XX syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) [OMIM
XX 223900]. It was found that mutations in the IKBKAP gene (see ABQ80565)
XX are associated with FD. The mutation associated with the major haplotype
XX of FD, FDI mutation, is a base pair (bp) mutation, where the thymine
XX nucleotide located at bp 6 of intron 20 in the IKBKAP gene is replaced
XX with a cytosine. This results in skipping of exon 20 in the mRNA from FD
XX patients, although they continue to express varying levels of wild-type
XX message in a tissue-specific manner. The mutation associated with the
XX minor haplotype, FD2 mutation, is a bp mutation, where the guanine
XX nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a cytosine.
XX This bp mutation causes an arginine to proline missense mutation (R696P)
XX in the IKBKAP protein, which is predicted to disrupt a potential
XX phosphorylation site. The IKBKAP nucleic acid sequences are useful for
XX identifying a subject with FD and for rapid carrier screening. The IKBKAP
XX gene contains 37 exons and maps to chromosome 9q31. Note: the present
XX sequence was not shown in the specification, but was derived from the
XX human wild-type IKBKAP sequence given in Fig 6
XX
XX Sequence 66479 BP; 18271 A; 12399 C; 14129 G; 21680 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 18; DB 6; Length 66479;
XX Best Local Similarity 100.0%; Pred. NO. 33;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ATGCTTGCTACTTGGCTG 18
DB 33818 ATGCTTGCTACTTGGCTG 33801

RESULT 4
ABQ80568/c
ID ABQ80568 standard; DNA; 66479 BP.
XX
AC ABQ80568;
XX
XX 08-NOV-2002 (first entry)
XX
XX Mutant human IKBKAP gene #3.
XX
XX Human; IKBKAP; Familial Dysautonomia; FD; Riley-Day syndrome;
XX Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening;
XX FDI; mutation; gene; chromosome 9q31; ds.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX mutation replace(33714,G)
XX FT /*tag= a
XX FT mutation
XX FT replace(34201,T)
XX FT /*tag= b
XX
XX WO200259381-A2.
XX
XX 01-AUG-2002.
XX
XX 07-JAN-2002; 2002WO-US000473.
XX
XX 06-JAN-2001; 2001US-0260080P.
XX

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PA (GEO) GEN HOSPITAL CORP.  
 XX  
 PI Slaughenhaupt S, Gusella JF;  
 XX WPI; 2002-674806/72.  
 DR  
 XX  
 XX New IKKAP genes with mutations, useful for identifying a subject with  
 PT familial dysautonomia (FD), or for rapid carrier screening in the  
 PT Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or  
 PT prenatal diagnosis.  
 XX  
 XX Claim 1; Page; 109pp; English.  
 PS  
 XX The present invention relates to methods and compositions useful for  
 CC detecting mutations which cause Familial Dysautonomia (FD, Riley-Day  
 CC syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) [OMIM  
 CC 223900]. It was found that mutations in the IKKAP gene (see AB080565)  
 CC are associated with FD. The mutation associated with the major haplotype  
 CC of FD, FDI mutation, is a base pair (bp) mutation, where the thymine  
 CC nucleotide located at bp 6 of intron 20 in the IKKAP gene is replaced  
 CC with a cytosine. This results in skipping of exon 20 in the mRNA from FD  
 CC patients, although they continue to express varying levels of wild-type  
 CC message in a tissue-specific manner. The mutation associated with the  
 CC minor haplotype, FD2 mutation, is a bp mutation, where the guanine  
 CC nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a cytosine.  
 CC This bp mutation causes an arginine to proline missense mutation (R696P)  
 CC in the IKKAP protein, which is predicted to disrupt a potential  
 CC phosphorylation site. The IKKAP nucleic acid sequences are useful for  
 CC identifying a subject with FD and for rapid carrier screening. The IKKAP  
 CC gene contains 37 exons and maps to chromosome 9q31. Note: the present  
 CC sequence was not shown in the specification, but was derived from the  
 CC human wild-type IKKAP sequence given in Fig 6  
 XX  
 SQ Sequence 66479 BP; 18271 A; 12400 C; 14128 G; 21680 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 18; DB 6; Length 66479;  
 Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1 ATGCTTGACTTGCTG 18  
 |||||  
 DB 33818 ATGCTTGACTTGCTG 33801  
 RESULT 5  
 ABQ80565/c  
 ID ABQ80565 standard; DNA; 66479 BP.  
 XX  
 AC ABQ80565;  
 XX  
 DT 08-NOV-2002 (first entry)  
 XX  
 DE Human IKKAP wild-type gene.  
 XX  
 XX Human; IKKAP; Familial Dysautonomia; FD; Riley-Day syndrome;  
 KW Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening;  
 KW gene; chromosome 9q31; ds.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200259381-A2.  
 PN  
 XX 01-AUG-2002.  
 PD  
 XX 07-JAN-2002; 2002WO-US000473.  
 PF  
 XX 06-JAN-2001; 2001US-026080P.  
 PR  
 XX (GEO) GEN HOSPITAL CORP.  
 PA  
 XX Slaughenhaupt S, Gusella JF;  
 PI WPI; 2002-674806/72.  
 DR

XX  
 XX New IKKAP genes with mutations, useful for identifying a subject with  
 PT familial dysautonomia (FD), or for rapid carrier screening in the  
 PT Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or  
 PT prenatal diagnosis.  
 XX  
 XX Claim 1; Fig 6; 109pp; English.  
 PS  
 XX The present invention relates to methods and compositions useful for  
 CC detecting mutations which cause Familial Dysautonomia (FD, Riley-Day  
 CC syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) [OMIM  
 CC 223900]. It was found that mutations in the IKKAP gene (the present  
 CC sequence) are associated with FD. The mutation associated with the major  
 CC haplotype of FD, FDI mutation, is a base pair (bp) mutation, where the  
 CC thymine nucleotide located at bp 6 of intron 20 in the IKKAP gene is  
 CC replaced with a cytosine. This results in skipping of exon 20 in the mRNA  
 CC from FD patients, although they continue to express varying levels of  
 CC wild-type message in a tissue-specific manner. The mutation associated  
 CC with the minor haplotype, FD2 mutation, is a bp mutation, where the  
 CC guanine nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a  
 CC cytosine. This bp mutation causes an arginine to proline missense  
 CC mutation (R696P) in the IKKAP protein, which is predicted to disrupt a  
 CC potential phosphorylation site. The IKKAP nucleic acid sequences are  
 CC useful for identifying a subject with FD and for rapid carrier screening.  
 CC The IKKAP gene contains 37 exons and maps to chromosome 9q31  
 XX  
 SQ Sequence 66479 BP; 18271 A; 12398 C; 14129 G; 21681 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 18; DB 6; Length 66479;  
 Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1 ATGCTTGACTTGCTG 18  
 |||||  
 DB 33818 ATGCTTGACTTGCTG 33801  
 RESULT 6  
 ACF67663  
 ID ACF67663 standard; DNA; 201 BP.  
 XX  
 AC ACF67663;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Photorhabdus luminescens nucleotide sequence #6130.  
 XX  
 KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;  
 KW detection; food; gene expression; plant; animal; microorganism; toxin;  
 KW antibiotic; biopesticide; virulence factor; disease model; plague;  
 KW whooping cough; gene; ds.  
 XX  
 OS Photorhabdus luminescens.  
 XX  
 XX WO200294867-A2.  
 PN  
 XX 28-NOV-2002.  
 PD  
 XX 07-FEB-2002; 2002WO-IB003040.  
 PF  
 XX 07-FEB-2001; 2001FR-00001659.  
 PR  
 XX (INSP) INST PASTEUR.  
 PA (CNRS) CNRS CENT NAT RECH SCI.  
 XX  
 XX Duchaud E, Tacurit S, Glaser P, Frangeul L, Kunst F, Danchin A;  
 PI Buchrieser C;  
 PI WPI; 2003-148459/14.  
 DR  
 XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,  
 PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.  
 XX

PS Claim 2; SEQ ID NO 6130; 1205pp; French.

XX The invention relates to the isolation of genes and their encoded

CC proteins from Photobacterium luminescens. The isolated sequences are

CC sources of probes and primers for detecting the genome of P. luminescens

CC and related species; to study polymorphisms; for gene analysis and for

CC detection/amplification of the genes. Antibodies (Ab) raised against the

CC polypeptides encoded by the genes are used for detection/identification

CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that

CC carry a gene-containing vector are used to select compounds that

CC modulate, regulate, induce or inhibit expression of the genes in plants,

CC animals or microorganisms other than P. luminescens and are able to alter

CC response or sensitivity to toxins and antibiotics produced by P.

CC recombinant production of the proteins, particularly toxins and

CC antibacterials useful as insecticides, bactericides and fungicides. The

CC genes, proteins, vectors containing the genes and Ab are also useful

CC therapeutically (to treat microbial infection by bacteria or fungi that

CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as

CC biopesticides. Other uses of the genes and the proteins are as virulence

CC factors and for identifying targets of human diseases for which P.

CC luminescens is a model (particularly plague and whooping cough). This

CC sequence represents one of the isolated P. luminescens genes

XX

SQ Sequence 201 BP; 64 A; 29 C; 48 G; 60 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 10; Length 201;

Best Local Similarity 94.4%; Pred. No. 1.4e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGCTACTTGCTG 18

Db 38 ATGCTTGCTACTTGCTG 55

RESULT 7

ACF65423/c

ID ACP65423 standard; DNA; 751 BP.

XX

AC ACP65423;

XX

DT 20-NOV-2003 (first entry)

XX

DE Photobacterium luminescens nucleotide sequence #3890.

XX

XX Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;

XX detection; food; gene expression; plant; animal; microorganism; toxin;

XX antibiotic; biopesticide; virulence factor; disease model; plague;

XX whooping cough; gene; ds.

XX

OS Photobacterium luminescens.

XX

PN WO200294867-A2.

XX

PD 28-NOV-2002.

XX

XX 07-FEB-2002; 2002WO-IB003040.

PF

XX 07-FEB-2001; 2001FR-00001659.

PR

XX (INSP ) INST PASTEUR

PA (CNRS ) CNRS CENT NAT RECH SCI.

XX

XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;

PI Buchrieser C;

PI WPI; 2003-148459/14.

DR

XX Genomic sequence of Photobacterium luminescens and encoded polypeptides,

PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.

XX

XX Claim 28; SEQ ID NO 3890; 1205pp; French.

PS

XX

CC The invention relates to the isolation of genes and their encoded

CC proteins from Photobacterium luminescens. The isolated sequences are

CC sources of probes and primers for detecting the genome of P. luminescens

CC and related species; to study polymorphisms; for gene analysis and for

CC detection/amplification of the genes. Antibodies (Ab) raised against the

CC polypeptides encoded by the genes are used for detection/identification

CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that

CC carry a gene-containing vector are used to select compounds that

CC modulate, regulate, induce or inhibit expression of the genes in plants,

CC animals or microorganisms other than P. luminescens and are able to alter

CC response or sensitivity to toxins and antibiotics produced by P.

CC recombinant production of the proteins, particularly toxins and

CC antibacterials useful as insecticides, bactericides and fungicides. The

CC genes, proteins, vectors containing the genes and Ab are also useful

CC therapeutically (to treat microbial infection by bacteria or fungi that

CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as

CC biopesticides. Other uses of the genes and the proteins are as virulence

CC factors and for identifying targets of human diseases for which P.

CC luminescens is a model (particularly plague and whooping cough). This

CC sequence represents one of the isolated P. luminescens genes

XX

SQ Sequence 751 BP; 215 A; 237 C; 101 G; 197 T; 0 U; 1 Other;

Query Match 91.1%; Score 16.4; DB 10; Length 751;

Best Local Similarity 94.4%; Pred. No. 1.6e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGCTACTTGCTG 18

Db 95 ATGCTTGCTACTTGCTG 78

RESULT 8

ADA31773

ID ADA31773 standard; DNA; 1122 BP.

XX

AC ADA31773;

XX

DT 20-NOV-2003 (first entry)

XX

DE DNA encoding Acinetobacter baumannii protein #3060.

XX

XX ds; gene; Acinetobacter baumannii; bacterial disease; antibacterial;

XX vaccine; plant biocontrol agent.

XX

OS Acinetobacter baumannii.

XX

PN US6562958-B1.

XX

PD 13-MAY-2003.

XX

XX 04-JUN-1999; 99US-00328352.

PF

XX 09-JUN-1998; 98US-0088701P.

PR

XX (GENO-) GENOME THERAPEUTICS CORP.

PA

XX Breton G, Bush D;

PI

XX WPI; 2003-576092/54.

DR

XX P-PSDB; ADA35899.

XX

XX New Acinetobacter baumannii proteins and nucleic acids, useful as reagents

PT for diagnosing a bacterial disease, as components of antibacterial

PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for

PT plants.

XX

XX Example; SEQ ID NO 3060; 328pp; English.

PS

XX The invention relates to isolated Acinetobacter baumannii nucleic acids.

XX The A. baumannii nucleic acids and polypeptides are useful as reagents

CC for diagnosing a bacterial disease, as components of antibacterial

CC

CC vaccines, as targets for antibacterial drugs, to detect the presence of  
CC A. baumannii and other Acinetobacter species in a sample, in screening  
CC compounds for the ability to interfere with the A. baumannii life cycle  
CC or to inhibit A. baumannii infection, and as biocontrol agents for  
CC plants. The present sequence represents DNA encoding an A. baumannii  
CC protein.  
CC  
XX  
SQ Sequence 1122 BP; 334 A; 197 C; 238 G; 353 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 9; Length 1122;  
Best Local Similarity 94.4%; Pred. No. 1.6e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGGTACTTGCTG 18  
|||||  
Db 764 ATGCTTGGTACTTGCTG 781  
|||||

RESULT 9  
ABL06290  
ID ABL06290 standard; cDNA; 13629 BP.

AC ABL06290;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 13352.

XX Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical; gene; ss.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

DR P-PSDB; ABB62187.

XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signaling and cell-cell  
PT interactions.

XX Claim 1; SEQ ID NO 13352; 21bp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA  
CC sequences (AB101840-AB116175) and the encoded proteins (ABB57737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13629 BP; 3397 A; 3369 C; 3256 G; 3607 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 4; Length 13629;  
Best Local Similarity 94.4%; Pred. No. 1.9e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGGTACTTGCTG 18

Db 10704 ATGCTTGGTACTTGCTG 10721  
|||||

RESULT 10

ACF65383\_1  
Continuation (2 of 5) of ACF65383 from base 100001 (Photorhabdus luminescens nucleotide  
WP Sequence split into 5 fragments LOCUS ACF65383 Accession ACF65383

WP	Fragment Name	Begin	End
WP	ACF65383_0	1	110000
WP	ACF65383_1	100001	210000
WP	ACF65383_2	200001	310000
WP	ACF65383_3	300001	410000
WP	ACF65383_4	400001	460203

Query Match 91.1%; Score 16.4; DB 10; Length 110000;  
Best Local Similarity 94.4%; Pred. No. 2.3e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGGTACTTGCTG 18  
|||||

Db 93035 ATGCTTGGTACTTGCTG 93052

RESULT 11  
ACF67367\_02

Continuation (3 of 57) of ACF67367 from base 200001 (Photorhabdus luminescens nucleotide  
WP Sequence split into 57 fragments LOCUS ACF67367 Accession ACF67367

WP	Fragment Name	Begin	End
WP	ACF67367_00	1	110000
WP	ACF67367_01	100001	210000
WP	ACF67367_02	200001	310000
WP	ACF67367_03	300001	410000
WP	ACF67367_04	400001	510000
WP	ACF67367_05	500001	610000
WP	ACF67367_06	600001	710000
WP	ACF67367_07	700001	810000
WP	ACF67367_08	800001	910000
WP	ACF67367_09	900001	1010000
WP	ACF67367_10	1000001	1110000
WP	ACF67367_11	1100001	1210000
WP	ACF67367_12	1200001	1310000
WP	ACF67367_13	1300001	1410000
WP	ACF67367_14	1400001	1510000
WP	ACF67367_15	1500001	1610000
WP	ACF67367_16	1600001	1710000
WP	ACF67367_17	1700001	1810000
WP	ACF67367_18	1800001	1910000
WP	ACF67367_19	1900001	2010000
WP	ACF67367_20	2000001	2110000
WP	ACF67367_21	2100001	2210000
WP	ACF67367_22	2200001	2310000
WP	ACF67367_23	2300001	2410000
WP	ACF67367_24	2400001	2510000
WP	ACF67367_25	2500001	2610000
WP	ACF67367_26	2600001	2710000
WP	ACF67367_27	2700001	2810000
WP	ACF67367_28	2800001	2910000
WP	ACF67367_29	2900001	3010000
WP	ACF67367_30	3000001	3110000
WP	ACF67367_31	3100001	3210000
WP	ACF67367_32	3200001	3310000
WP	ACF67367_33	3300001	3410000
WP	ACF67367_34	3400001	3510000
WP	ACF67367_35	3500001	3610000
WP	ACF67367_36	3600001	3710000
WP	ACF67367_37	3700001	3810000
WP	ACF67367_38	3800001	3910000
WP	ACF67367_39	3900001	4010000
WP	ACF67367_40	4000001	4100000
WP	ACF67367_41	4100001	4210000
WP	ACF67367_42	4200001	4310000
WP	ACF67367_43	4300001	4410000

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WP ACF67367_44 4400001 4510000
WP ACF67367_45 4500001 4610000
WP ACF67367_46 4600001 4710000
WP ACF67367_47 4700001 4810000
WP ACF67367_48 4800001 4910000
WP ACF67367_49 4900001 5010000
WP ACF67367_50 5000001 5110000
WP ACF67367_51 5100001 5210000
WP ACF67367_52 5200001 5310000
WP ACF67367_53 5300001 5410000
WP ACF67367_54 5400001 5510000
WP ACF67367_55 5500001 5610000
WP ACF67367_56 5600001 5648894

Query Match 91.1%; Score 16.4; DB 10; Length 110000;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGGTACTTGGCTG 18
    |||||
Db 60513 ATGCTTGGTATTGGCTG 60530

RESULT 12
ABN69291
ID ABN69291 standard; DNA; 1074 BP.
AC ABN69291;
XX
XX 01-JUL-2002 (first entry)
XX
DE Streptococcus polynucleotide SEQ ID NO 6495.
XX
KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW group A streptococcus; Streptococcus pyogenes; antibacterial; gene;
KW antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
XX
OS Streptococcus pyogenes.
XX
XX WO200234771-A2.
XX
XX 02-MAY-2002.
XX
XX 29-OCT-2001; 2001WO-GB004789.
XX
XX 27-OCT-2000; 2000GB-00026333.
XX
XX 24-NOV-2000; 2000GB-00028727.
XX
XX 07-MAR-2001; 2001GB-00005640.
XX
XX (CHIR-) CHIRON SPA.
XX
XX (GENO-) INST GENOMIC RES.
XX
XX Telford J, Massignani V, Margarit Y, Rosi, Grandi G, Fraser C;
XX Tettelin H;
XX
XX WPI; 2002-352536/38.
XX
XX P-PSDB; ABP28660.
XX
XX New Streptococcus protein for the treatment or prevention of infection or
XX disease caused by Streptococcus bacteria, such as meningitis, and for
XX detecting a compound that binds to the protein.
XX
XX Claim 7; Page 3812; 4525pp; English.
XX
XX The invention relates to a protein (ABP25413-ABP30895) from group B
XX streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
XX (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
XX the specification. The proteins have antibacterial and antiinflammatory
XX activity. (i), nucleic acids encoding (i), ABN6044-ABN71526 and
XX antibodies that bind (i) are used in the manufacture of medicaments for
XX the treatment or prevention of infection or disease caused by
XX Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
XX Nucleic acids encoding (i) are used to detect Streptococcus in a
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CC biological sample. (I) is used to determine whether a compound binds to
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (I) may be used to recombinantly produce (I) and may be
CC used in gene therapy. Antibodies to (I) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins
XX
SQ Sequence 1074 BP; 308 A; 170 C; 211 G; 395 T; 0 U; 0 Other;
Query Match 85.6%; Score 15.4; DB 6; Length 1074;
Best Local Similarity 94.1%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TCGTTGGTACTTGGCTG 18
    |||||
Db 908 TGCTAGGTACTTGGCTG 924

RESULT 13
ACF71824
ID ACF71824 standard; DNA; 3045 BP.
XX
XX ACF71824;
XX
XX 20-NOV-2003 (first entry)
XX
DE Photorhabdus luminescens nucleotide sequence #10291.
XX
KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KW detection; food; gene expression; plant; animal; microorganism; toxin;
KW antibiotic; bioplastic; virulence factor; disease model; plague;
KW whooping cough; gene; ds.
XX
OS Photorhabdus luminescens.
XX
XX WO200294867-A2.
XX
XX 28-NOV-2002.
XX
XX 07-FEB-2002; 2002WO-IB003040.
XX
XX 07-FEB-2001; 2001FR-00001659.
XX
XX (INSP ) INST PASTEUR.
XX
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
XX Buchrieser C;
XX
XX WPI; 2003-148459/14.
XX
XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
XX useful e.g. as therapeutic antimicrobials and agricultural pesticides.
XX
XX Claim 2; SEQ ID NO 10291; 1205pp; French.
XX
XX The invention relates to the isolation of genes and their encoded
XX proteins from Photorhabdus luminescens. The isolated sequences are
XX sources of probes and primers for detecting the genome of P. luminescens
XX and related species; to study polymorphisms; for gene analysis and for
XX detection/amplification of the genes. Antibodies (Ab) raised against the
XX polypeptides encoded by the genes are used for detection/identification
XX of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
XX carry a gene-containing vector are used to select compounds that
XX modulate, regulate, induce or inhibit expression of the genes in plants,
XX animals or microorganisms other than P. luminescens and are able to alter
XX response or sensitivity to toxins and antibiotics produced by P.
XX luminescens. Cells transformed to express the genes are useful for
XX recombinant production of the proteins, particularly toxins and
XX antibacterials useful as insecticides, bactericides and fungicides. The
XX genes, proteins, vectors containing the genes and Ab are also useful
```

CC therapeutically (to treat microbial infection by bacteria or fungi that  
 CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as  
 CC biopesticides. Other uses of the genes and the proteins are as virulence  
 CC factors and for identifying targets of human diseases for which P.  
 CC luminescens is a model (particularly plague and whooping cough). This  
 CC sequence represents one of the isolated P. luminescens genes  
 XX

SQ Sequence 3045 BP; 923 A; 504 C; 707 G; 911 T; 0 U; 0 Other;  
 Query Match 85.6%; Score 15.4; DB 10; Length 3045;  
 Best Local Similarity 94.1%; Pred. No. 5.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTGGCT 17  
 |||||  
 Db 1070 ATACTTGCTACTGGCT 1086

RESULT 14  
 ACD13393  
 ID ACD13393 standard; cDNA; 15382 BP.

AC ACD13393;

DT 13-AUG-2003 (first entry)

DE Human DNA encoding a p53 modifier, SEQ ID 64.

KW Human; ss; Gene; p53 modifier; cytostatic; cancer; cytostatic;  
 KW antiangiogenic; antiapoptotic; p53 pathway; breast cancer; colon cancer;  
 KW kidney cancer; lung cancer; ovarian cancer; angiogenesis; cell cycle;  
 KW apoptotic disorder; cell proliferation disorder.

OS Homo sapiens.

PN WO200299122-A1.

PD 12-DEC-2002.

PF 03-JUN-2002; 2002WO-US017382.

PR 05-JUN-2001; 2001US-0296076P.

PR 10-OCT-2001; 2001US-0328605P.

PR 15-FEB-2002; 2002US-0357263P.

PA (EXEL-) EXELIXIS INC.

PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;  
 DR WPI; 2003-156859/15.  
 DR P-PSDB; ABO07219.

XX Identifying modulators of the p53 pathway for use in treating apoptotic  
 PT or cell proliferation disorders, comprises screening for agents that  
 PT modulate activity of a human ortholog of genes that modify the p53  
 PT pathway in Drosophila.

PS Example 2; Page 314-318; 678pp; English.

XX The invention relates to identifying (M1) a candidate p53 pathway  
 CC modulating agent, by contacting an assay system comprising a purified HM  
 CC polypeptide (human ortholog of genes that modify the p53 pathway in  
 CC Drosophila) or nucleic acid with a test agent under conditions, where but  
 CC for the presence of the test agent, the system provides a reference  
 CC activity, and detecting a test agent-biased activity of the assay system.  
 CC Also included are modulating (M2) a p53 pathway of a cell (comprising  
 CC contacting a cell defective in p53 function with a candidate modulator  
 CC that specifically binds to a HM polypeptide comprising an HM amino acid  
 CC sequence, where p53 function is restored), modulating (M3) a p53 pathway  
 CC in a mammalian cell (comprising contacting the cell with an agent that  
 CC specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)  
 CC a disease in a patient (comprising: (a) obtaining a biological sample  
 CC from the patient; (b) contacting the sample with a probe for HM

CC expression; (c) comparing the results with a control; and (d) determining  
 CC whether the comparison indicates a likelihood disease). (M1) is useful  
 CC for identifying modulators of the p53 pathway. A probe for HM expression  
 CC is useful for diagnosing breast, colon, kidney, lung and ovarian cancer,  
 CC in a patient, where the cancer has greater than 25 % expression level.  
 CC Modulators identified by (M1) are useful in a variety of diagnostic and  
 CC therapeutic applications, where disease or disorder prognosis is related  
 CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell  
 CC proliferation disorders (e.g. cancer). Another two new methods (M2 and  
 CC M3) are useful for modulating the p53 pathway of a cell, thus restoring  
 CC the p53 function of the cell, so that the cell undergoes normal  
 CC proliferation or progression through the cell cycle. (M2) and (M3) are  
 CC also useful for treating defects in the p53 pathway such as angiogenic,  
 CC apoptotic or cell proliferation disorders. The present sequence is an HM  
 CC nucleic acid encoding a p53 pathway modifying protein  
 XX

SQ Sequence 15382 BP; 2970 A; 4184 C; 4737 G; 3491 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 8; Length 15382;  
 Best Local Similarity 94.1%; Pred. No. 6.4e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTGGCT 17  
 |||||  
 Db 10596 ATGCTTGCTACTGGCT 10612

RESULT 15

ACF67367\_50

Continuation (51 of 57) of ACF67367 from base 5000001 (Photothabdus luminescens nucleotic  
 WP Sequence split into 57 fragments LOCUS ACF67367 Accession ACF67367

WP	Fragment Name	Begin	End
WP	ACF67367_00	1	110000
WP	ACF67367_01	100001	210000
WP	ACF67367_02	200001	310000
WP	ACF67367_03	300001	410000
WP	ACF67367_04	400001	510000
WP	ACF67367_05	500001	610000
WP	ACF67367_06	600001	710000
WP	ACF67367_07	700001	810000
WP	ACF67367_08	800001	910000
WP	ACF67367_09	900001	1010000
WP	ACF67367_10	10000001	1110000
WP	ACF67367_11	11000001	1210000
WP	ACF67367_12	12000001	1310000
WP	ACF67367_13	13000001	1410000
WP	ACF67367_14	14000001	1510000
WP	ACF67367_15	15000001	1610000
WP	ACF67367_16	16000001	1710000
WP	ACF67367_17	17000001	1810000
WP	ACF67367_18	18000001	1910000
WP	ACF67367_19	19000001	2010000
WP	ACF67367_20	20000001	2110000
WP	ACF67367_21	21000001	2210000
WP	ACF67367_22	22000001	2310000
WP	ACF67367_23	23000001	2410000
WP	ACF67367_24	24000001	2510000
WP	ACF67367_25	25000001	2610000
WP	ACF67367_26	26000001	2710000
WP	ACF67367_27	27000001	2810000
WP	ACF67367_28	28000001	2910000
WP	ACF67367_29	29000001	3010000
WP	ACF67367_30	30000001	3110000
WP	ACF67367_31	31000001	3210000
WP	ACF67367_32	32000001	3310000
WP	ACF67367_33	33000001	3410000
WP	ACF67367_34	34000001	3510000
WP	ACF67367_35	35000001	3610000
WP	ACF67367_36	36000001	3710000
WP	ACF67367_37	37000001	3810000
WP	ACF67367_38	38000001	3910000
WP	ACF67367_39	39000001	4010000
WP	ACF67367_40	40000001	4110000

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WP ACF67367_41 4100001 4210000
WP ACF67367_42 4200001 4310000
WP ACF67367_43 4300001 4410000
WP ACF67367_44 4400001 4510000
WP ACF67367_45 4500001 4610000
WP ACF67367_46 4600001 4710000
WP ACF67367_47 4700001 4810000
WP ACF67367_48 4800001 4910000
WP ACF67367_49 4900001 5010000
WP ACF67367_50 5000001 5110000
WP ACF67367_51 5100001 5210000
WP ACF67367_52 5200001 5310000
WP ACF67367_53 5300001 5410000
WP ACF67367_54 5400001 5510000
WP ACF67367_55 5500001 5610000
WP ACF67367_56 5600001 5648894

Query Match 85.6%; Score 15.4; DB 10; Length 110000;
Best Local Similarity 94.1%; Pred. No. 7.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGGTACTTGGCT 17
||| ||||| ||||| |||||
Db 67525 ATACTTGGTACTTGGCT 67541

RESULT 16
ACF65387_1
Continuation (2 of 7) of ACF65387 from base 100001 (Photorhabdus luminescens nucleotide
WP Sequence split into 7 fragments LOCUS ACF65387 Accession ACF65387
WP Fragment Name Begin End
WP ACF65387_0 1 110000
WP ACF65387_1 100001 210000
WP ACF65387_2 200001 310000
WP ACF65387_3 300001 410000
WP ACF65387_4 400001 510000
WP ACF65387_5 500001 610000
WP ACF65387_6 600001 696798

Query Match 85.6%; Score 15.4; DB 10; Length 110000;
Best Local Similarity 94.1%; Pred. No. 7.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGGTACTTGGCT 17
||| ||||| ||||| |||||
Db 107039 ATACTTGGTACTTGGCT 107055

RESULT 17
ACF65387_2
Continuation (3 of 7) of ACF65387 from base 200001 (Photorhabdus luminescens nucleotide
WP Sequence split into 7 fragments LOCUS ACF65387 Accession ACF65387
WP Fragment Name Begin End
WP ACF65387_0 1 110000
WP ACF65387_1 100001 210000
WP ACF65387_2 200001 310000
WP ACF65387_3 300001 410000
WP ACF65387_4 400001 510000
WP ACF65387_5 500001 610000
WP ACF65387_6 600001 696798

Query Match 85.6%; Score 15.4; DB 10; Length 110000;
Best Local Similarity 94.1%; Pred. No. 7.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGGTACTTGGCT 17
||| ||||| ||||| |||||
Db 7039 ATACTTGGTACTTGGCT 7055

RESULT 18
ABL59091
ID ABL59091 standard; DNA; 112414 BP.
```

```
XX ABL59091;
AC 4310000
XX 07-AUG-2003 (revised)
DT 20-AUG-2002 (first entry)
XX
DE Nucleotide sequence of Ehime-1 strain of Red sea bream iridovirus.
XX
KW Neutralisation; Chrysophrys major iridovirus; antigen; RSIV; ss.
XX
OS Red sea bream iridovirus.
XX
PN JP2002101885-A.
XX
PD 09-APR-2002.
XX
XX 27-SEP-2000; 2000JP-00294991.
PR 27-SEP-2000; 2000JP-00294991.
XX
PA (NORQ ) NORINSUISANSHO YOSHOKU KENKYU.
PA (KURI/) KURITA J.
XX
XX WPI; 2002-440455/47.
XX
PT A DNA encoding a protein related to neutralization and infection
PT prevention of Chrysophrys major iridovirus.
XX
PS Example 1; Page 13-51; 65pp; Japanese.
XX
CC The specification describes proteins related to neutralisation and
CC infection prevention of Chrysophrys major iridovirus. The protein encoded
CC by the DNA is useful as an antigen for preventing infection of the
CC Chrysophrys major iridovirus. The present sequence represents the
CC nucleotide sequence of the Ehime-1 strain of Red sea bream iridovirus
CC (RSIV). (Updated on 07-AUG-2003 to correct OS field.)
XX
XX Sequence 112414 BP; 26205 A; 29684 C; 30351 G; 26174 T; 0 U; 0 Other;
SQ

Query Match 85.6%; Score 15.4; DB 6; Length 112414;
Best Local Similarity 94.1%; Pred. No. 7.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGCTTGGTACTTGGCTG 18
||||| ||||| ||||| |||||
Db 102187 TGCTTGGTACTTGGCGG 102203

RESULT 19
ADO43653
ID ADO43653 standard; DNA; 127432 BP.
XX
AC ADO43653;
XX
XX 29-JUL-2004 (first entry)
XX
DE Nucleotide sequence of BAC-64.
XX
KW pentatricopeptide sequence; PPR sequence; ppr-A; ppr-B; ppr-C;
KW male fertility; plant; Rfo locus; radish; Brassica; cytoplasmic inducer;
KW BAC; primer; ss.
XX
OS Synthetic.
XX
XX WO2004039988-A1.
XX
XX 13-MAY-2004.
XX
XX 29-OCT-2003; 2003WO-FR003224.
XX
XX 29-OCT-2002; 2002FR-00013512.
XX
XX (GENO-) GENOPLANTE-VALOR.
```

XX PI Budar F, Giancola S, Bendahmane A, Desloire S, Delourme R;  
PI Marhadour S, Falentin-Guyomarc'h H, Falentin C, Renard M, Gherbi H;  
PI Laloui W, Bonden S, Wilmer J, Clouet V;  
XX WPI; 2004-376197/35.  
DR New pentatricopeptides from plants, useful for restoration of male  
XX fertility in Brassica containing cytoplasmic inducer of male sterility,  
PT especially for production of colza hybrids, also related nucleic acids.  
XX Example 1; Page 67-102; 106pp; French.  
PS The present sequence represents bacterial artificial chromosome (BAC)-64.  
XX This BAC contains the rfo locus, which contains pentatricopeptide (PPR)  
CC sequences. The specification describes PPR sequences, designated ppr-A,  
CC ppr-B and ppr-C. These PPR sequences are able to restore male fertility  
CC in plant. PPR sequences, used singly or in combination, are used to  
CC restore male fertility in Brassica, specifically B. napus, that contain a  
CC cytoplasmic inducer of male sterility. The plants with restored fertility  
CC are used for production of hybrids.  
XX SQ Sequence 127432 BP; 42300 A; 21940 C; 21537 G; 40004 T; 0 U; 1651 Other;  
Query Match 85.6%; Score 15.4; DB 12; Length 127432;  
Best Local Similarity 94.1%; Pred. No. 7.3e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGCTTGCTACTGGCT 17  
Db 75338 ATGCTTGCTACTGGCT 75354  
RESULT 20  
ADP65796/c  
ID ADP65796 standard; DNA; 270150 BP.  
XX AC ADP65796;  
XX DT 12-AUG-2004 (first entry)  
XX DE Human 16p133 sequence section 7 of 8 DNA.  
XX KW autoimmune disease; arthritis; gene expression analysis;  
KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;  
KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;  
KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;  
KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;  
KW immune; ds; human.  
XX OS Homo sapiens.  
XX PN WO2003072827-A1.  
XX PD 04-SEP-2003.  
XX PF 31-OCT-2002; 2002WO-US035433.  
XX PR 31-OCT-2001; 2001US-0336220P.  
XX PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
XX PI Hirsch R, Thorton SL;  
XX WPI; 2003-712740/67.  
XX DR GENEANK; AE006639, AE005175.  
XX PT Diagnosing and analyzing autoimmune disease using gene expression  
PT profiles and microarray technology, useful for diagnosing and treating  
PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and  
PT gout.  
XX Disclosure; Page; 56pp; English.

XX The invention relates to a novel method for diagnosing and analysing  
CC autoimmune disease or arthritides. The method comprises obtaining a  
CC patient sample containing mRNA, analysing gene expression using the mRNA  
CC that results in a gene expression signature of the mRNA, and using that  
CC gene expression signature to diagnose or analyse the autoimmune disease  
CC or arthritides in the patient, where gene expression of at least 60% of  
CC the genes correlates with that of the gene signature. The invention  
CC further comprises: a treatment of rheumatoid arthritis; identification of  
CC genes for targeting in the treatment of rheumatoid arthritis in a mammal;  
CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an  
CC array or gene chip, specific for rheumatoid arthritis; diagnosis or  
CC analyses of autoimmune disease or rheumatoid arthritis; screening the  
CC efficacy of a candidate drug in vitro for the treatment of collagen-  
CC induced arthritis; and reducing the symptoms associated with collagen-  
CC induced arthritis. The compositions of the invention have the following  
CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,  
CC antigout, antiinflammatory, dermatological, and immunomodulatory. The  
CC methods and compositions of the present invention are useful for  
CC diagnosing and treating autoimmune disease or arthritides, such as  
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,  
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an  
CC immune disease caused by an infectious agent. This polynucleotide, and  
CC represents a DNA sequence relating to the genes used in the analysis and  
CC treatment of autoimmune diseases or arthritides. Note: This sequence is  
CC not shown in the specification. It has been supplied in an electronic  
CC format from WIPO.  
XX SQ Sequence 270150 BP; 61621 A; 70689 C; 71725 G; 64903 T; 0 U; 1212 Other;  
Query Match 85.6%; Score 15.4; DB 11; Length 270150;  
Best Local Similarity 94.1%; Pred. No. 7.7e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 TCGTTGGTACTGGCTG 18  
Db 31854 TCGTGGTACTGGCTG 31838  
RESULT 21  
ADD25213  
ID ADD25213 standard; DNA; 271990 BP.  
XX AC ADD25213;  
XX DT 15-JAN-2004 (first entry)  
XX DE Fertility restorer protein genomic DNA sequence.  
XX KW fertility restorer protein; male sterile plant; viable pollen production;  
KW selection marker; ds; gene.  
XX OS Unidentified.  
XX PN WO2003006622-A2.  
XX PD 23-JAN-2003.  
XX PF 12-JUL-2002; 2002WO-US022217.  
XX PR 12-JUL-2001; 2001US-0305026P.  
XX PR 13-JUL-2001; 2001US-0305363P.  
XX PR 30-JUL-2001; 2001US-0308736P.  
XX PA (UYMC-) UNIV MCGILL.  
XX PA (DNAL-) DNA LANDMARKS INC.  
XX PI Brown GG, Formanova N, Dendy C, Landry BS, Cheung W, Jin H;  
XX WPI; 2003-221734/21.  
XX PT New nuclear fertility restorer genes, useful for restoring fertility in  
PT cytoplasmic male-sterile plants such as Brassica napus plants, or for



PT increasing production of viable pollen in a plant.

XX Claim 1; SEQ ID NO 87; 191pp; English.

XX The invention comprises the amino acid and coding sequences of isolated

CC fertility restorer proteins. The DNA and protein sequences of the

CC invention are useful for restoring fertility in male sterile plants, such

CC as Brassica napus plants. The DNA and protein sequences of the invention

CC are useful for increasing production of viable pollen in a plant. The DNA

CC and protein sequences are also useful as selection markers to identify

CC transformed plant cells. The present genomic DNA sequence contains coding

XX sequences for fertility restorer proteins of the invention.

SQ Sequence 271990 BP; 89597 A; 47325 C; 46930 G; 88078 T; 0 U; 60 Other;

Query Match 85.6%; Score 15.4; DB 10; Length 271990;

Best Local Similarity 94.1%; Pred. No. 7.7e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGGTACTTGGCT 17

Db 154736 ATGCTTGATCTTGGCT 154752

RESULT 22

ADN61228

ID ADN61228 standard; DNA; 271990 BP.

XX AC ADN61228;

XX DT 01-JUL-2004 (first entry)

XX DE Radish nuclear fertility restorer Rfo Rfo locus SEQ ID NO:87.

XX KW nuclear fertility; plant; male-fertility; male-fertility restorer;

XX KW marker; transformation; radish; Rfo; Petunia; Rf; Brassica napus; ds;

XX KW gene.

XX OS Raphanus sativum.

XX PN WO2004006655-A2.

XX PD 22-JAN-2004.

XX PF 16-JAN-2003; 2003WO-US001343.

XX PR 12-JUL-2002; 2002US-00195144.

XX PR 15-JAN-2003; 2003US-00345072.

XX PA (UVMC-) UNIV MCGILL.

XX PA (DNAL-) DNA LANDMARKS INC.

XX PA (BADI ) BASF PLANT SCI GMBH.

XX PI Brown GG, Formanova N, Deny C, Landry BS, Cheung W, Jin H;

XX PI Lai FM, Leforest M;

XX DR WPI; 2004-122713/12.

XX Using a plant male-fertility restorer as a marker for transformation by

PT providing an expression cassette encoding a plant male fertility restorer

PT and transforming cytoplasmic male sterile plant cells with the expression

PT cassette.

XX Claim 15; SEQ ID NO 87; 309pp; English.

XX The invention relates to a novel method for using a plant male-fertility

CC restorer as a marker for transformation. Using a plant male-fertility

CC restorer as a marker for transformation comprises: providing an

CC expression cassette for a male fertility restorer; transforming

CC cytoplasmic male sterile plants with the expression cassette; and

CC identifying plants from step (2) that form seeds when self-pollinated.

CC The male fertility restorer is a radish Rfo or a petunia Rf. The plant is

CC Brassica napus. The expression cassette is covalently linked to a

CC sequence of interest. The expression cassette is co-transformed into the

CC plant cells with a nucleotide sequence of interest. The method is useful

CC for using a plant male-fertility restorer as a marker for transformation.

CC The present sequence is used in the exemplification of the invention.

XX SQ Sequence 271990 BP; 89601 A; 47321 C; 46931 G; 88077 T; 0 U; 60 Other;

Query Match 85.6%; Score 15.4; DB 12; Length 271990;

Best Local Similarity 94.1%; Pred. No. 7.7e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGGTACTTGGCT 17

Db 154736 ATGCTTGATCTTGGCT 154752

RESULT 23

ADC87619/c

ID ADC87619 standard; DNA; 349981 BP.

XX AC ADC87619;

XX DT 01-JAN-2004 (first entry)

XX DE Human GPCR related polynucleotide SEQ ID NO:2072.

XX KW ds; human; GPCR; guanosine triphosphate-binding protein coupled receptor;

XX KW gene therapy.

XX OS Homo sapiens.

XX PN EP1270724-A2.

XX PD 02-JAN-2003.

XX PF 18-JUN-2002; 2002EP-00013517.

XX PR 18-JUN-2001; 2001JP-00246789.

XX PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

XX PI Suwa M, Asai K, Akiyama Y, Aburatani H;

XX WPI; 2003-315783/31.

XX New polynucleotide, useful for preparing a composition for treating a

PT patient in need of increased or suppressed activity or expression of the

PT guanosine triphosphate-binding protein coupled receptor.

XX Disclosure; SEQ ID NO 2072; 28pp; English.

XX The invention relates to a novel polynucleotide encoding a guanosine

CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of

CC the invention may have a use in gene therapy. The polynucleotide and

CC polypeptide are useful for preparing a composition for treating a patient

CC in need of increased or suppressed activity or expression of the

CC guanosine triphosphate-binding protein coupled receptor. The protein

CC sequences shown in ADC87618-ADC87623 represent polynucleotide sequences

CC related to the invention.

XX SQ Sequence 349981 BP; 100900 A; 78560 C; 77396 G; 92823 T; 0 U; 302 Other;

Query Match 85.6%; Score 15.4; DB 10; Length 349981;

Best Local Similarity 94.1%; Pred. No. 7.8e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TCCTTGGTACTTGGCTG 18

Db 135745 TCCTTGGGACTTGGCTG 135729

RESULT 24



XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.  
KW Homo sapiens.  
OS  
XX EP1074617-A2.  
XX  
XX 07-FEB-2001.  
XX  
XX 28-JUL-2000; 2000EP-00116126.  
XX  
XX 29-JUL-1999; 99JP-00248036.  
PR 27-AUG-1999; 99JP-00300253.  
PR 11-JAN-2000; 2000JP-00118776.  
PR 02-MAY-2000; 2000JP-00183767.  
PR 03-JUN-2000; 2000JP-00241899.  
XX  
XX (HELI-) HELIX RES INST.  
XX  
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
XX  
XX WPI; 2001-318749/34.  
XX  
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.  
XX  
XX Claim 1; SEQ ID NO 2010; 2537pp + Sequence Listing; English.  
XX  
XX The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises:  
CC (a) an oligo-dT primer and an oligonucleotide complementary to the  
CC complementary strand of a polynucleotide which comprises one of the 5602  
CC nucleotide sequences defined in the specification, where the  
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
CC of an oligonucleotide comprising a sequence complementary to the  
CC complementary strand of a polynucleotide which comprises a 5'-end  
CC sequence and an oligonucleotide comprising a sequence complementary to a  
CC polynucleotide which comprises a 3'-end sequence, where the  
CC oligonucleotide comprises at least 15 nucleotides and the combination of  
CC the 5'-end sequence/3'-end sequence is selected from those defined in the  
CC specification. The primer sets can be used in antisense therapy and in  
CC gene therapy. The primers are useful for synthesizing polynucleotides,  
CC particularly full-length cDNAs. The primers are also useful for the  
CC detection and/or diagnosis of the abnormality of the proteins encoded by  
CC the full-length cDNAs. The primers allow obtaining of the full-length  
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893  
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent  
CC polynucleotides, all of which are used in the exemplification of the  
CC present invention  
XX  
XX Sequence 884 BP; 245 A; 177 C; 170 G; 279 T; 0 U; 13 Other;  
SQ  
Query Match 83.3%; Score 15; DB 4; Length 884;  
Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 TGCTGGTACTGGC 16  
DB 110 TGCTGGTACTGGC 124  
RESULT 27  
ADE86815/c  
ID ADE86815 standard; cDNA; 2351 BP.  
XX  
AC ADE86815;  
XX  
XX 29-JAN-2004 (first entry)  
XX

DE Petunia PEIL3 nucleic acid sequence.  
XX  
XX ss; ethylene insensitive; EIN2; abscission; EIN3; transgenic plant;  
KW flower abscission zone-specific promoter; Arabidopsis; petunia; lettuce;  
KW tomato; geranium; begonia; cotton; food source; fibre; pharmaceutical;  
KW flower longevity; PEIL2; PEIL1; PEIL3.  
XX  
XX Petunia x hybrida.  
XX  
XX Key Location/Qualifiers  
FH CDS 240..2078  
FT /\*tag= a  
FT /product= "PEIL3"  
XX  
XX WO2003088738-A1.  
PN  
XX 30-OCT-2003.  
PD  
XX 22-APR-2003; 2003WO-US012409.  
PF  
XX 22-APR-2002; 2002US-037455SP.  
PR 28-OCT-2002; 2002WO-US034566.  
PR  
XX (PLAN-) PLANTGENIX INC.  
PA  
XX Ciardi J, Cibulsky RJ, Clark D, Nourizadeh S, Tieman D;  
PI WPI; 2003-854009/79.  
XX P-PSDB; ADE86842.  
DR  
XX Controlling abscission in a transformed, commercially useful plants, e.g.  
PT flowering plants, and food source plants, useful for enhancing flower  
PT longevity, comprises overexpressing EIN2 and/or EIN3 genes in the  
PT transgenic plants.  
XX  
XX Disclosure; SEQ ID NO 8; 136pp; English.  
PS  
XX This sequence represents the Petunia EIN3-like protein, PEIL3, nucleic  
CC acid sequence. This sequence is one of the preferred nucleic acid  
CC sequences for use in the method of the invention for controlling  
CC abscission in a transformed, commercially useful plant. The method  
CC comprising effecting the overexpression of EIN2 and/or EIN3 in the  
CC resulting transgenic plant as compared with a non-transformed wild type  
CC plant. Overexpression of the EIN2 gene may be driven with a flower  
CC abscission zone-specific promoter, where the overexpressed EIN2 gene has  
CC at least 50% identity to the EIN2 gene in Arabidopsis. The preferred  
CC nucleic acid sequences are petunia, lettuce, tomato, geranium, begonia,  
CC or cotton EIN2. The method is useful for controlling abscission in a  
CC transformed, commercially useful plants such as flowering plants, food  
CC source plants, and other commercially useful plants for the production of  
CC fibres or pharmaceuticals. EIN2 and/or EIN3 are useful for enhancing  
CC flower longevity, and for reducing flower abscission. The petunia EIN3  
CC genes was antisense in petunia under transcriptional control of the  
CC constitutive CAMV 35S promoter. One of the genes, PEIL2, was also  
CC overexpressed under the control of the CAMV 35S promoter. Over 70  
CC transgenic lines were produced for each construct. Only plants that were  
CC overexpressing PEIL2 displayed an increase in flower longevity up to 9  
CC days after gassing and 6 days after pollination compared to 1.5 days and  
CC 2 days, respectively, for wild type flowers. Antisense expression of each  
CC gene had no effect.  
XX  
XX Sequence 2351 BP; 700 A; 450 C; 545 G; 656 T; 0 U; 0 Other;  
SQ  
Query Match 83.3%; Score 15; DB 10; Length 2351;  
Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GCTTGGTACTGGCT 17  
DB 715 GCTTGGTACTGGCT 701  
RESULT 28

RESULT 29  
AAC56059/C  
ID AAC56059 standard; DNA; 2444 BP.  
XX AC AC  
XX AAC56059;  
DT 25-JAN-2001 (first entry)  
XX XX  
DE Eucalyptus grandis transcription factor DNA sequence #190.  
XX XX  
KW plant; transcription factor; gene expression; eucalyptus; pine; acacia;  
KW poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;  
KW basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;  
KW homeodomain zipper; LIM domain; AP2; ERBs; zinc finger domain;  
KW type 2 Cys2His2; CCAAT box element; MYB; ss.  
XX XX  
OS Eucalyptus grandis.  
XX OS  
PN WQ200053724-A2.  
XX PN  
XX 14-SEP-2000.  
PD PD  
XX XX  
PF 09-MAR-2000; 200OWO-US006112.  
XX PF  
PR 11-MAR-1999; 99US-00266513.  
XX PR  
PR 18-AUG-1999; 99US-0149485P.  
XX PR  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
XX PA  
PI Wood M, McGrath A, Shenk MA, Glenn M;  
XX PI  
XX WPI; 2000-579369/54.  
DR DR  
XX XX  
PT New isolated polynucleotide encoding a plant transcription factor for  
PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,  
FT having modified gene expression or modified activity of a polypeptide.  
XX FT  
XX Claim 1; page 94-95; 747pp; English.

The present invention relates to novel plant transcription factors from  
Eucalyptus grandis or Pinus radiata. The present sequence is the coding  
sequence for one such transcription factor. The transcription factor may  
be used to produce a plant having modified gene expression such as a  
woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or  
mahogany species or to modify the activity of a polypeptide in a plant.  
The transcription factors of the present invention are members from the  
following families of regulatory proteins: bZIP, bZIP family of G-box  
binding factors, basic helix-loop-helix zipper,  
homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2  
and ERBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements and  
MYB

Sequence 2444 BP; 643 A; 554 C; 640 G; 607 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 3; Length 2444;  
Best Local Similarity 100.0%; Pred. No. 8.9e-02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 3 GCTTGGTACTGGCT 17  
DB 740 GCTTGGTACTGGCT 726  
|||||  
|||||

RESULT 30  
AAD07786  
ID AAD07786 standard; cDNA; 2988 BP.  
XX AC  
XX AAD07786;  
XX AC  
XX AAD07786;  
DT 10-AUG-2001 (first entry)  
XX XX  
DE Human secreted protein-encoding gene 4 cDNA clone HAGEB14 SEQ ID NO:27.

XX Human; secreted protein; proliferative disorder; cancer; tumour;  
KW foetal abnormality; developmental abnormality; haematopoietic disorder;  
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
KW inflammation; allergy; neurological disorder; Alzheimer's disease;  
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;  
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;  
KW cardiovascular disorder; angioinfectious disorder; kidney disorder;  
KW gastrointestinal disorder; pregnancy-related disorder;  
KW endocrine disorder; infection; wound healing; vulnerability; cell culture;  
KW chemotaxis; food additive; gene therapy; binding partner identification;  
KW SS.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1344..1601  
FT /\*tag= a  
FT /product= "Human secreted protein precursor"  
FT sig\_peptide 1344..1454  
FT /\*tag= b  
FT mat\_peptide 1455..1598  
FT /\*tag= c  
FT /product= "Human secreted protein"  
XX WO200132587-A1.  
XX 10-MAY-2001.  
XX 25-OCT-2000; 2000WO-US029364.  
XX 29-OCT-1999; 99US-0162238P.  
XX 30-JUN-2000; 2000US-0215134P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Ruben SM, Komatsoulis GA, Duan RD, Fiscella M, Ebner R;  
PI WPI; 2001-308740/32.  
DR P-PSDB; AAE03394.  
XX  
XX Isolated nucleic acid molecule encoding a human secreted protein is used  
XX in preventing, treating or ameliorating a medical condition.  
XX  
XX Claim 1; Page 358; 398pp; English.  
XX  
XX AAD07770-AAD07794 represent cDNAs corresponding to 10 human secreted  
XX protein genes, and AAE03378-AAE03402 represent the proteins they encode.  
XX AAE03403-AAE03415 represent human secreted protein fragments or variants.  
XX The secreted proteins and their genes are useful for preventing, treating  
XX or ameliorating medical conditions, e.g., by protein or gene therapy.  
XX Pathological conditions can be diagnosed by determining the amount of the  
XX new protein in a sample or by determining the presence of mutations in  
XX the new genes. Specific uses are described for each of the 10 genes,  
XX based on the tissues in which they are most highly expressed, and include  
XX developing products for the diagnosis or treatment of proliferative  
XX disorders, cancer, tumours, foetal and developmental abnormalities,  
XX haematopoietic disorders, diseases of the immune system, AIDS, autoimmune  
XX diseases (e.g., rheumatoid arthritis), inflammation, allergies,  
XX neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),  
XX cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,  
XX psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,  
XX angioinfectious disorders, kidney disorders, gastrointestinal disorders,  
XX pregnancy-related disorders, endocrine disorders, and infections. The  
XX proteins can also be used to aid wound healing and epithelial cell  
XX proliferation, to prevent skin ageing due to sunburn, to maintain organs  
XX before transplantation, for supporting cell culture of primary tissues,  
XX to regenerate tissues, to identify their cognate ligands or binding  
XX partners, and in chemotaxis, and can be used as a food additive or  
XX preservative to modify storage properties. Antibodies specific for a  
XX protein of the invention can be used in alleviating symptoms associated  
XX with the disorders mentioned above, and in diagnostic immunoassays e.g.,  
XX radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The

CC present sequence represents a human secreted protein-encoding cDNA of the  
CC invention  
XX  
SQ Sequence 2988 BP; 725 A; 612 C; 749 G; 902 T; 0 U; 0 Other;  
Query Match 83.3%; Score 15; DB 4; Length 2988;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
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Db 639 TGCCTGGTACTTGGC 653  
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XX  
AC AAD34081;  
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DT 16-JUL-2002 (first entry)  
XX  
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XX  
KW Human; secreted protein; immunodeficiency; inflammation; septic shock;  
KW reperfusion injury; inflammatory bowel disease; autoimmune disorder;  
KW rheumatoid arthritis; gastrointestinal disorder; respiratory disorder;  
KW asthma; allergy; cancer; multiple sclerosis; cardiovascular disorder;  
KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;  
KW atherosclerosis; acquired immune deficiency syndrome; prion disease;  
KW AIDS-related dementia; hepatitis; blood-related disorder; thrombosis;  
KW hyperproliferative disorder; renal disorder; acute glomerulonephritis;  
KW endocrine disorder; Addison's disease; reproductive system disorder;  
KW endometriosis; infectious disease; pancreatic disorder; gene therapy;  
KW vaccine; gene; SS.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
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FT /product= "Human secreted protein precursor"  
FT sig\_peptide 1350..1454  
FT /\*tag= b  
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FT /product= "Human mature secreted protein"  
XX  
XX WO200216576-A1.  
XX  
XX 28-FEB-2002.  
XX  
XX 17-JAN-2001; 2001WO-US001396.  
XX  
XX 18-AUG-2000; 2000US-0226280P.  
XX 21-DEC-2000; 2000US-0256968P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Sopet DR;  
XX Olsen HS, Moore PA, Wei P, Ebner R, Duan RD, Shi Y, Choi GH;  
XX Fiscella M, Ni J;  
XX WPI; 2002-315464/35.  
XX P-PSDB; AAE21642.  
XX  
XX Human secreted polypeptides and polynucleotides for diagnosing,  
XX prognosing, preventing and treating immune, hyperproliferative, liver,  
XX kidney, and reproductive disorders and for identifying their modulators  
XX for therapeutic use.  
XX  
XX Claim 1; Page 414-415; 462pp; English.  
XX  
XX

CC AAD34068-AAD34096 represent cDNAs corresponding to 11 human secreted  
 CC protein genes, and AAE21629-AAE21657 represent the proteins they encode.  
 CC AAE21658-AAE21663 represent human secreted protein fragments. The genes  
 CC and their corresponding secreted proteins are useful for preventing,  
 CC treating or ameliorating medical conditions, e.g., by protein or gene  
 CC therapy. Pathological conditions can be diagnosed by determining the  
 CC amount of the new protein in a sample or by determining the presence of  
 CC mutations in the new genes. Specific uses are described for each of the  
 CC 11 genes, based on the tissues in which they are most highly expressed.  
 CC Sequences of the invention are useful in treating, preventing, diagnosing  
 CC and/or prognosing immunodeficiencies, inflammatory conditions (e.g.,  
 CC septic shock, reperfusion injury, inflammatory bowel disease), autoimmune  
 CC disorders (e.g., rheumatoid arthritis), gastrointestinal disorders,  
 CC respiratory disorders (e.g., asthma and allergy), cancers (e.g. liver and  
 CC breast), central nervous system (CNS) disorders (e.g., multiple  
 CC sclerosis), cardiovascular disorders (e.g., atherosclerosis), neuro-  
 CC degenerative disorders (e.g., Parkinson's disease, Alzheimer's disease,  
 CC AIDS-related dementia, prion disease) and many additional diseases,  
 CC conditions and disorders that are characterised by inflammation (e.g.,  
 CC hepatitis). They are also useful for treating blood-related disorder  
 CC (e.g., thrombosis), hyperproliferative disorders, renal disorders (e.g.,  
 CC acute glomerulonephritis), endocrine disorders (e.g., Addison's disease),  
 CC reproductive system disorders (e.g., endometriosis), infectious diseases  
 CC and pancreatic disorders. They are also useful as vaccine adjuvants that  
 CC enhance immune responsiveness to an antigen and as adjuvants to enhance  
 CC tumour-specific immune responses, anti-viral, anti-bacterial, anti-fungal  
 CC and anti-parasitic immune responses. Secreted proteins of the invention  
 CC are used for enhancing or inhibiting complement mediated cell lysis, for  
 CC stimulating wound and tissue repair, angiogenesis and the repair of  
 CC vascular or lymphatic diseases or disorders. They stimulate neuronal  
 CC growth and are used to treat, prevent and/or diagnose neuronal damage, to  
 CC prevent hair loss, to stimulate keratinocyte growth, to modulate  
 CC mammalian characteristics such as body height, weight, hair colour and to  
 CC increase or decrease storage capabilities, fat content, lipid, protein,  
 CC vitamins, carbohydrate, minerals, cofactors or other nutritional  
 CC components. Sequences of the invention are also useful in gene therapy.  
 CC The present sequence represents a human secreted protein-encoding cDNA of  
 CC the invention

XX SQ Sequence 2988 BP; 725 A; 612 C; 749 G; 902 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 6; Length 2988;  
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QY 2 TGCTTGGTACTTGGC 16  
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 Db 639 TGCTTGGTACTTGGC 653

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 AC AAD34069;  
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 DT 16-JUL-2002 (first entry)  
 XX  
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 KW Human; secreted protein; immunodeficiency; inflammation; septic shock;  
 KW reperfusion injury; inflammatory bowel disease; autoimmune disorder;  
 KW rheumatoid arthritis; gastrointestinal disorder; respiratory disorder;  
 KW asthma; allergy; cancer; multiple sclerosis; cardiovascular disorder;  
 KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;  
 KW atherosclerosis; acquired immune deficiency syndrome; prion disease;  
 KW AIDS-related dementia; hepatitis; blood-related disorder; thrombosis;  
 KW hyperproliferative disorder; renal disorder; acute glomerulonephritis;  
 KW endocrine disorder; Addison's disease; reproductive system disorder;  
 KW endometriosis; infectious diseases; pancreatic disorder; gene therapy;  
 KW vaccine; gene; ss.  
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 XX Homo sapiens.

XX Location/Qualifiers  
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 XX  
 PN WO200216576-A1.  
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 XX 28-FEB-2002.  
 XX  
 XX 17-JAN-2001; 2001WO-US001396.  
 XX  
 XX 18-AUG-2000; 2000US-0226280P.  
 XX 21-DEC-2000; 2000US-0258968P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Komatsoulis CA, Baker KP, Birse CE, Soppet DR;  
 PI Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH;  
 PI Piscella M, Ni J;  
 PI  
 XX WPI; 2002-315464/35.  
 DR P-PSDB; AAE21630.  
 XX  
 XX Human secreted polypeptides and polynucleotides for diagnosing,  
 XX prognosing, preventing and treating immune, hyperproliferative, liver,  
 XX kidney, and reproductive disorders and for identifying their modulators  
 XX for therapeutic use.  
 XX  
 XX Claim 1; Page 404-405; 462pp; English.  
 XX  
 XX AAD34068-AAD34096 represent cDNAs corresponding to 11 human secreted  
 CC protein genes, and AAE21629-AAE21657 represent the proteins they encode.  
 CC AAE21658-AAE21663 represent human secreted protein fragments. The genes  
 CC and their corresponding secreted proteins are useful for preventing,  
 CC treating or ameliorating medical conditions, e.g., by protein or gene  
 CC therapy. Pathological conditions can be diagnosed by determining the  
 CC amount of the new protein in a sample or by determining the presence of  
 CC mutations in the new genes. Specific uses are described for each of the  
 CC 11 genes, based on the tissues in which they are most highly expressed.  
 CC Sequences of the invention are useful in treating, preventing, diagnosing  
 CC and/or prognosing immunodeficiencies, inflammatory conditions (e.g.,  
 CC septic shock, reperfusion injury, inflammatory bowel disease), autoimmune  
 CC disorders (e.g., rheumatoid arthritis), inflammatory bowel diseases,  
 CC respiratory disorders (e.g., asthma and allergy), cancers (e.g. liver and  
 CC breast), central nervous system (CNS) disorders (e.g., Addison's disease),  
 CC sclerosis, cardiovascular disorders (e.g., atherosclerosis), neuro-  
 CC degenerative disorders (e.g., Parkinson's disease, Alzheimer's disease,  
 CC AIDS-related dementia, prion disease) and many additional diseases,  
 CC conditions and disorders that are characterised by inflammation (e.g.,  
 CC hepatitis). They are also useful for treating blood-related disorder  
 CC (e.g., thrombosis), hyperproliferative disorders, renal disorders (e.g.,  
 CC acute glomerulonephritis), endocrine disorders (e.g., Addison's disease),  
 CC reproductive system disorders (e.g., endometriosis), infectious diseases  
 CC and pancreatic disorders. They are also useful as vaccine adjuvants that  
 CC enhance immune responsiveness to an antigen and as adjuvants to enhance  
 CC tumour-specific immune responses, anti-viral, anti-bacterial, anti-fungal  
 CC and anti-parasitic immune responses. Secreted proteins of the invention  
 CC are used for enhancing or inhibiting complement mediated cell lysis, for  
 CC stimulating wound and tissue repair, angiogenesis and the repair of  
 CC vascular or lymphatic diseases or disorders. They stimulate neuronal  
 CC growth and are used to treat, prevent and/or diagnose neuronal damage, to  
 CC prevent hair loss, to stimulate keratinocyte growth, to modulate  
 CC mammalian characteristics such as body height, weight, hair colour and to  
 CC increase or decrease storage capabilities, fat content, lipid, protein,  
 CC vitamins, carbohydrate, minerals, cofactors or other nutritional  
 CC components. Sequences of the invention are also useful in gene therapy.  
 CC The present sequence represents a human secreted protein-encoding cDNA of  
 CC the invention

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CC the invention
XX
SQ Sequence 3283 BP; 777 A; 678 C; 851 G; 977 T; 0 U; 0 Other;

  Query Match      83.3%; Score 15; DB 6; Length 3283;
  Best Local Similarity 100.0%; Pred. No. 9.1e+02;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGCTTGGTACTTGGC 16
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Db 934 TGCTTGGTACTTGGC 948

RESULT 33
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AC AAD34080;
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XX
XX Human; secreted protein; immunodeficiency; inflammation; septic shock;
XX reperfusion injury; inflammatory bowel disease; autoimmune disorder;
XX rheumatoid arthritis; gastrointestinal disorder; respiratory disorder;
XX asthma; allergy; cancer; multiple sclerosis; cardiovascular disorder;
XX neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
XX atherosclerosis; acquired immune deficiency syndrome; prion disease;
XX AIDS-related dementia; hepatitis; blood-related disorder; thrombosis;
XX hyperproliferative disorder; renal disorder; acute glomerulonephritis;
XX endocrine disorder; Addison's disease; reproductive system disorder;
XX endometriosis; infectious disease; pancreatic disorder; gene therapy;
XX vaccine; gene; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH sig_peptide 1645..1749
FT /*tag= b
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XX
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XX 28-FEB-2002.
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XX 21-DEC-2000; 2000US-0256968P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Komatsculis GA, Baker KP, Birse CE, Soppet DR,
XX Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH;
XX Fiscella M, Ni J;
XX
XX WPI; 2002-315464/35.
XX P-PSDB; AAE21641.
XX
XX Human secreted polypeptides and polynucleotides for diagnosing,
XX prognosing, preventing and treating immune, hyperproliferative, liver,
XX kidney, and reproductive disorders and for identifying their modulators
XX for therapeutic use.
XX
XX Claim 1; Page 413-414; 462pp; English.
XX
XX AAD34068-AAD34096 represent cDNAs corresponding to 11 human secreted
XX

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CC protein genes, and AAE21629-AAE21657 represent the proteins they encode.
CC AAE21658-AAE21663 represent human secreted protein fragments. The genes
CC and their corresponding secreted proteins are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Pathological conditions can be diagnosed by determining the
CC amount of the new protein in a sample or by determining the presence of
CC mutations in the new genes. Specific uses are described for each of the
CC 11 genes, based on the tissues in which they are most highly expressed.
CC Sequences of the invention are useful in treating, preventing, diagnosing
CC and/or prognosing immunodeficiencies, inflammatory conditions (e.g.,
CC septic shock, reperfusion injury, inflammatory bowel disease), autoimmune
CC disorders (e.g., rheumatoid arthritis), gastrointestinal disorders,
CC respiratory disorders (e.g., asthma and allergy), cancers (e.g. liver and
CC breast), central nervous system (CNS) disorders (e.g., multiple
CC sclerosis), cardiovascular disorders (e.g., atherosclerosis), neuro-
CC degenerative disorders (e.g., Parkinson's disease, Alzheimer's disease,
CC AIDS-related dementia, prion disease) and many additional diseases,
CC Conditions and disorders that are characterised by inflammation (e.g.,
CC hepatitis). They are also useful for treating blood-related disorder
CC (e.g., thrombosis), hyperproliferative disorders, renal disorders (e.g.,
CC acute glomerulonephritis), endocrine disorders (e.g., Addison's disease),
CC and pancreatic disorders. They are also useful as vaccine adjuvants that
CC enhance immune responsiveness to an antigen and as adjuvants to enhance
CC tumour-specific immune responses, anti-viral, anti-bacterial, anti-fungal
CC and anti-parasitic immune responses. Secreted proteins of the invention
CC are used for enhancing or inhibiting complement mediated cell lysis, for
CC stimulating wound and tissue repair, angiogenesis and the repair of
CC vascular or lymphatic diseases or disorders. They stimulate neuronal
CC growth and are used to treat, prevent and/or diagnose neuronal damage, to
CC prevent hair loss, to stimulate keratinocyte growth, to modulate
CC mammalian characteristics such as body height, weight, hair colour and to
CC increase or decrease storage capabilities, fat content, lipid, protein,
CC vitamins, carbohydrate, minerals, cofactors or other nutritional
CC components. Sequences of the invention are also useful in gene therapy.
CC The present sequence represents a human secreted protein-encoding cDNA of
CC the invention
XX
XX SQ Sequence 3283 BP; 777 A; 678 C; 851 G; 977 T; 0 U; 0 Other;

  Query Match      83.3%; Score 15; DB 6; Length 3283;
  Best Local Similarity 100.0%; Pred. No. 9.1e+02;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 934 TGCTTGGTACTTGGC 948

RESULT 34
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XX 23-JAN-2002 (first entry)
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XX Human; nootropic; neuroprotective; cyrostatic; dermatological; virucide;
XX immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
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XX antirheumatic; hepatotropic; cerebrotective; antiinflammatory;
XX antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
XX antiparasitic; cardiac; immune disorder; cardiovascular disorder;
XX neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
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XX 16-AUG-2001.
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PF 17-JAN-2001; 2001WO-US001334.  
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PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228944P.  
PR 01-SEP-2000; 2000US-0229287P.  
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PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
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PR 17-NOV-2000; 2000US-0249265P.  
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PR 01-DEC-2000; 2000US-0250391P.  
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PR 08-DEC-2000; 2000US-0251989P.  
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PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX  
(HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX WPI; 2001-541565/60.  
XX  
XX Nucleic acids encoding 324 human nervous system antigen polypeptides,  
PR



PT useful for preventing, diagnosing and/or treating nervous system cancers  
PT and metastases.  
XX  
PS Disclosure; SEQ ID NO 10040; 1701pp + Sequence Listing; English.  
XX  
CC The invention relates to novel genes (ABA11004-ABA21534) and proteins  
CC (ABBA14678-ABBA18001) useful for preventing, treating or ameliorating  
CC medical conditions e.g. by protein or gene therapy. The genes are  
CC isolated from a range of human tissues disclosed in the specification.  
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in  
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,  
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune  
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)  
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing  
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)  
CC infectious diseases such as viral, bacterial, fungal and parasitic  
CC infections. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
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KW pharmacogenomic marker; gene; ss.  
XX  
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XX  
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PD 23-AUG-2001.  
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PF 20-FEB-2001; 2001WO-US005171.  
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PR 16-MAR-2000; 2000US-0189862P.  
PR 25-MAY-2000; 2000US-0207454P.  
PR 09-JUN-2000; 2000US-0211314P.  
PR 18-JUL-2000; 2000US-0219007P.  
PR 13-DEC-2000; 2000US-0255281P.  
XX  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
PI Schlegel R, Endege WO, Morahan JE;  
XX  
DR WPI; 2001-662795/76.  
XX  
PT Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer.  
XX  
PS Claim 1; Page 4271-4272; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for: (a) assessing whether  
CC a patient is afflicted with prostate cancer; (b) monitoring the  
CC progression of prostate cancer in a patient; (c) assessing the efficacy  
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
CC determining whether prostate cancer has metastasized in a patient; (h)  
CC assessing the aggressiveness or indolence of prostate cancer in a patient  
CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker  
XX  
SQ Sequence 4584 BP; 1097 A; 975 C; 1205 G; 1291 T; 0 U; 16 Other;  
Query Match 83.3%; Score 15; DB 5; Length 4584;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 TGCTTGGTACTTGGC 16  
|||||  
Db 2630 TGCTTGGTACTTGGC 2644  
RESULT 36  
ABV29293  
ID ABV29293 standard; cDNA; 4584 BP.  
XX  
AC ABV29293;  
XX  
DT 16-SEP-2002 (first entry)  
XX  
DE Human prostate expression marker cDNA 29284.  
XX  
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KW pharmacogenomic marker; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200160860-A2.  
XX  
PD 23-AUG-2001.  
XX  
PF 20-FEB-2001; 2001WO-US005171.  
XX  
PR 17-FEB-2000; 2000US-0183319P.  
PR 16-MAR-2000; 2000US-0189862P.  
PR 25-MAY-2000; 2000US-0207454P.  
PR 09-JUN-2000; 2000US-0211314P.  
PR 18-JUL-2000; 2000US-0219007P.  
PR 13-DEC-2000; 2000US-0255281P.  
XX  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
PI Schlegel R, Endege WO, Morahan JE;  
XX  
DR WPI; 2001-662795/76.  
XX  
PT Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer.  
XX  
PS Claim 1; Page 6259-6260; 11750pp; English.  
XX  
CC The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for: (a) assessing whether  
CC a patient is afflicted with prostate cancer; (b) monitoring the  
CC progression of prostate cancer in a patient; (c) assessing the efficacy  
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC

CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
 CC determining whether prostate cancer has metastasized in a patient; (h)  
 CC assessing the aggressiveness or indolence of prostate cancer in a patient  
 CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker  
 XX  
 SQ Sequence 4584 BP; 1097 A; 975 C; 1205 G; 1291 T; 0 U; 16 Other;

Query Match 83.3%; Score 15; DB 5; Length 4584;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGCTTGGTACTTGGC 16  
 |||||  
 Db 2630 TGCTTGGTACTTGGC 2644

RESULT 37  
 ADL45673  
 ID ADL45673 standard; DNA; 5170 BP.  
 XX  
 AC ADL45673;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human ovarian cancer DNA marker #19563.

XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX Homo sapiens.

XX WO200170979-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009126.

XX 21-MAR-2000; 2000US-0131031P.

XX 25-MAY-2000; 2000US-0207124P.

XX 15-JUN-2000; 2000US-0211940P.

XX 07-JUL-2000; 2000US-0216820P.

XX 25-JUL-2000; 2000US-0220661P.

XX 21-DEC-2000; 2000US-0257672P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Lee J, Lillie J;  
 XX WPI; 2001-611502/70.

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian  
 XX cancer cells as compared to their normal non-cancerous ovarian cells are  
 XX used to characterize stage, grade, histological type of ovarian cancer.

XX Disclosure; SEQ ID NO 19563; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in  
 XX ovarian cancer cells as compared to their expression in normal (i.e. non-  
 XX cancerous) ovarian cells. The invention also relates to polypeptides  
 XX encoded by the markers, antibodies that selectively bind to the  
 XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk  
 XX of developing ovarian cancer involving inhibiting expression of a gene  
 XX corresponding to a marker of the invention and a method of treating a  
 XX patient afflicted with ovarian cancer comprising providing to cells of  
 XX the patient an antisense oligonucleotide complementary to a marker of the  
 XX invention. The markers are useful for assessing if a patient is afflicted  
 XX with ovarian cancer, which involves comparing the level of expression of  
 XX a marker in a patient sample and a normal level of expression of the  
 XX marker in a control non-ovarian cancer sample. A difference between the  
 XX expression levels indicates ovarian cancer. The level of expression of a  
 XX marker corresponds to a secreted protein or to a transcribed  
 XX polynucleotide or its portion. The level of expression of the marker is  
 XX assessed by detecting the presence in the sample, a protein or protein  
 XX fragment corresponding to the marker. The presence of protein or protein

CC fragment is detected using an antibody that specifically binds with the  
 CC protein or protein fragment. Alternatively, the level of expression of  
 CC the marker is assessed by detecting the presence of a transcribed  
 CC polynucleotide which anneals with the marker or anneals with a portion of  
 CC the polynucleotide comprising the marker, under stringent conditions. The  
 CC marker is also used for monitoring the progression of ovarian cancer in a  
 CC patient which involves detecting expression of the marker in a patient  
 CC sample at a first point in time, repeating the method at a subsequent  
 CC time and comparing the level of expression. The method is carried out  
 CC using an ovarian tissue sample. A composition comprising a marker,  
 CC polypeptide or antibody of the invention is used to treat ovarian cancer.  
 CC This sequence represents a human ovarian cancer DNA marker of the  
 CC invention. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX  
 SQ Sequence 5170 BP; 1288 A; 1098 C; 1326 G; 1444 T; 0 U; 14 Other;

Query Match 83.3%; Score 15; DB 5; Length 5170;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGCTTGGTACTTGGC 16  
 |||||  
 Db 2630 TGCTTGGTACTTGGC 2644

RESULT 38  
 ABL04480

ID ABL04480 standard; cDNA; 7120 BP.

XX  
 AC ABL04480;

XX  
 DT 26-MAR-2002 (first entry)

XX  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 7922.

XX Drosophila; developmental biology; cell signalling; insecticide;

XX pharmaceutical; gene; ss.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

XX 11-JUL-2000; 2000US-00614150.

XX (PEXE ) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX P-FSDS; ABB560377.

XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 XX genes from Drosophila and for elucidating cell signaling and cell-cell  
 XX interactions.

XX Claim 1; SEQ ID NO 7922; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent  
 XX capable of detecting 1000 or more genes from Drosophila. The invention is  
 XX useful in developmental biology and in elucidating cell signalling and  
 XX cell-cell interactions in higher eukaryotes for the development of  
 XX insecticides, therapeutics and pharmaceutical drugs. The invention  
 XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 XX sequences (ABL01840-ABL16175), and the encoded proteins (ABB57737-  
 XX ABB72072). The sequence data for this patent did not form part of the  
 XX printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 7120 BP; 1930 A; 1594 C; 1644 G; 1952 T; 0 U; 0 Other;  
SQ Query Match 83.3%; Score 15; DB 4; Length 7120;  
Best Local Similarity 100.0%; Pred. No. 9.6e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 CTGGTGGTACTGGCTG 18  
DB 3562 CTGGTGGTACTGGCTG 3576  
|||||  
ACF62736/c  
ID ACF62736 standard; DNA; 183610 BP.  
XX AC ACF62736;  
XX 08-OCT-2003 (first entry)  
XX Cancer based on CYP3A5 related polynucleotide SEQ ID NO:664.  
XX Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma;  
XX cytochrome p450; subfamily IIIA; nifedipine oxidase; polypeptide 5;  
XX cytosstatic; gene; ds.  
XX Unidentified.  
XX WO2003013534-A2.  
XX 20-FEB-2003.  
XX 23-JUL-2002; 2002WO-EP008219.  
XX 23-JUL-2001; 2001EP-00117608.  
XX 24-MAY-2002; 2002EP-00011710.  
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
XX Heinrich G, Kerb R;  
XX WPI; 2003-268144/26.  
XX New use of irinotecan for preparation of compositions for treating cancer  
XX in subject having genome with variant allele comprising cytochrome p450,  
XX subfamily IIIA, polypeptide 5 polynucleotide, termed CYP3A5.  
XX Disclosure; SEQ ID NO 664; 86pp; English.  
XX The present invention describes the use of irinotecan (I) or its  
XX derivative for the preparation of a pharmaceutical composition for  
XX treating colorectal, cervical, gastric, lung, ovarian or pancreatic  
XX cancer, or malignant glioma in a subject having a genome with a variant  
XX allele which comprises a cytochrome p450, subfamily IIIA (nifedipine  
XX oxidase), polypeptide 5 (CYP3A5) polynucleotide (II). (I) and (II) have  
XX cytostatic activity. The therapeutic applications of (I) is improved.  
XX since it is possible to individually treat a subject with an appropriate  
XX dosage and/or an appropriate derivative of (I). Therefore, undesirable,  
XX harmful or toxic effects are efficiently avoided. Unnecessary and  
XX potentially harmful treatment of those subjects who do not respond to the  
XX treatment with substances (nonresponders), as well as the development of  
XX drug resistances due to suboptimal drug dosing can be avoided. ACP62200  
XX to ACP62751 and ABM34912 to ABM35013 represent sequences used in the  
XX exemplification of the present invention  
SQ Sequence 183610 BP; 50187 A; 43907 C; 42684 G; 45427 T; 0 U; 1405 Other;  
  
Query Match 83.3%; Score 15; DB 8; Length 183610;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ATGCTTGGTACTTGG 15

DB 107647 ATGCTTGGTACTTGG 107633  
|||||  
RESULT 40  
ADB20851/c  
ID ADB20851 standard; DNA; 183610 BP.  
XX AC ADB20851;  
XX 20-NOV-2003 (first entry)  
XX MRP1 based cancer related nucleic acid SEQ ID NO:564.  
XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;  
XX lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;  
XX variant allele; multidrug resistance protein 1; MRP1; cytosstatic; gene;  
XX ds.  
XX Unidentified.  
XX WO2003013533-A2.  
XX 20-FEB-2003.  
XX 23-JUL-2002; 2002WO-EP008200.  
XX 23-JUL-2001; 2001EP-00117608.  
XX 24-MAY-2002; 2002EP-00011710.  
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
XX Heinrich G, Kerb R;  
XX WPI; 2003-354397/33.  
XX Use of irinotecan or its derivative for preparation of a pharmaceutical  
XX composition for treating cancer in a subject having a genome with a  
XX variant allele comprising a multidrug resistance protein 1  
XX polynucleotide.  
XX Disclosure; SEQ ID NO 664; 100pp; English.  
XX The present invention describes a method for the use of irinotecan (I) or  
XX its derivative for the preparation of a pharmaceutical composition for  
XX treating colorectal, cervical, gastric, lung, ovarian or pancreatic  
XX cancer, or malignant glioma in a subject having a genome with a variant  
XX allele which comprises a multidrug resistance protein 1 (MRP1)  
XX polynucleotide (II). (I) has cytostatic activity. (I) or its derivative  
XX can be used for the preparation of a pharmaceutical composition for  
XX treating colorectal, cervical, gastric, lung, ovarian or pancreatic  
XX cancer, or malignant glioma in a subject, where the subject is a human  
XX (preferably African or Asian) or a mouse. The present sequence represents  
XX a sequence which is used in the exemplification of the present invention.  
SQ Sequence 183610 BP; 50187 A; 43907 C; 42684 G; 45427 T; 0 U; 1405 Other;  
  
Query Match 83.3%; Score 15; DB 8; Length 183610;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ATGCTTGGTACTTGG 15  
DB 107647 ATGCTTGGTACTTGG 107633  
|||||  
RESULT 41  
ADB87940/c  
ID ADB87940 standard; DNA; 183610 BP.  
XX AC ADB87940;  
XX 04-DEC-2003 (first entry)

XX DE Human UGT1A1 gene sequence SEQ ID NO:664.  
XX DE  
XX irinotecan; cancer; UGT1A1; cytostatic; topoisomerase I inhibitor;  
KW colorectal cancer; cervical cancer; gastric cancer; lung cancer;  
KW ovarian cancer; pancreatic cancer; malignant glioma;  
KW uridine diphosphate glycosyltransferase member A1; gene; ds.  
XX OS  
XX Homo sapiens.  
XX PN WO2003013536-A2.  
XX XX  
XX PD 20-FEB-2003.  
XX XX  
XX PF 23-JUL-2002; 2002WO-EP008217.  
XX XX  
XX PR 23-JUL-2001; 2001EP-00117608.  
XX PR 24-MAY-2002; 2002EP-00011710.  
XX XX  
XX PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
XX PI Heinrich G, Kerb R;  
XX WPI; 2003-289896/28.  
XX DR  
XX XX  
XX Use of irinotecan to treat cancer patient by determining if patient has  
PT variant alleles of UGT1A1 gene, administering increased/decreased amounts  
PT of irinotecan based on increased/decreased levels of UGT1A1 gene product.  
XX PT  
XX PS Disclosure; SEQ ID NO 664; 107pp; English.  
XX XX  
XX The invention relates to the novel use of irinotecan to treat a patient  
CC suffering from cancer. This involves determining if the patient has one  
CC or more variant alleles of the UGT1A1 gene, and if the patient has one or  
CC more of such variant alleles, irinotecan is administered in an increased  
CC or decreased amount in comparison to the amount that is administered  
CC without regard to the patient's alleles in the UGT1A1 gene. The invention  
CC has cytostatic activity. A composition of the invention acts as a  
CC topoisomerase I inhibitor. The method is useful for treating a patient,  
CC an animal e.g. mouse or a human, preferably African or Asian, suffering  
CC from cancer such as colorectal, cervical, gastric cancer, lung, ovarian,  
CC pancreatic cancer or malignant glioma. The present sequence is used in  
CC the exemplification of the invention.  
XX XX  
XX Sequence 183610 BP; 50187 A; 43907 C; 42684 G; 45427 T; 0 U; 1405 Other;  
SQ  
Query Match 83.3%; Score 15; DB 10; Length 183610;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGCTTGCTACTGG 15  
Db 107647 ATGCTTGCTACTGG 107633  
RESULT 42  
ADB96923/C  
ID ADB96923 standard; DNA; 183610 BP.  
XX AC ADB96923;  
XX XX  
XX DT 04-DEC-2003 (first entry)  
XX DE Human MDR1 related DNA sequence SEQ ID NO:664.  
XX XX  
KW irinotecan; colorectal cancer; cervical cancer; gastric cancer;  
KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;  
KW multidrug resistance 1; MDR1; cytostatic; human; CYP3A5; MRP1; MDR1;  
KW TOP1; ds.  
XX OS  
XX Homo sapiens.  
XX PN WO2003013537-A2.  
XX XX

XX PD 20-FEB-2003.  
XX XX  
XX PF 23-JUL-2002; 2002WO-EP008218.  
XX XX  
XX PR 23-JUL-2001; 2001EP-00117608.  
XX PR 24-MAY-2002; 2002EP-00011710.  
XX XX  
XX PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
XX PI Heinrich G, Kerb R;  
XX WPI; 2003-268145/26.  
XX DR  
XX XX  
XX New use of irinotecan for preparation of pharmaceutical compositions for  
PT treating cancer in subject having genome with variant allele comprising  
PT multidrug resistance 1 polynucleotide.  
XX PT  
XX PS Disclosure; SEQ ID NO 664; 130pp; English.  
XX XX  
XX The invention relates to the novel use of irinotecan or its derivative  
CC for the preparation of pharmaceutical compositions for treating  
CC colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or  
CC malignant glioma in a subject having a genome with a variant allele which  
CC comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition  
CC of the invention has cytostatic activity. The invention is useful for the  
CC preparation of pharmaceutical compositions for treating colorectal,  
CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant  
CC glioma in a subject (preferably human, more preferably African or Asian)  
CC or a mouse. The present sequence is used in the exemplification of the  
CC invention.  
XX XX  
XX Sequence 183610 BP; 50187 A; 43907 C; 42684 G; 45427 T; 0 U; 1405 Other;  
SQ  
Query Match 83.3%; Score 15; DB 10; Length 183610;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGCTTGCTACTGG 15  
Db 107647 ATGCTTGCTACTGG 107633  
RESULT 43  
ADB92114/C  
ID ADB92114 standard; DNA; 183610 BP.  
XX AC ADB92114;  
XX XX  
XX DT 04-DEC-2003 (first entry)  
XX DE Human MDR1 related DNA sequence SEQ ID NO:664.  
XX XX  
KW irinotecan; colorectal cancer; cervical cancer; gastric cancer;  
KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;  
KW multidrug resistance 1; MDR1; cytostatic; human; UGT1A1; MRP1; TOP1; ds.  
XX OS  
XX Homo sapiens.  
XX PN WO2003013535-A2.  
XX XX  
XX PD 20-FEB-2003.  
XX XX  
XX PF 23-JUL-2002; 2002WO-EP008220.  
XX XX  
XX PR 23-JUL-2001; 2001EP-00117608.  
XX PR 24-MAY-2002; 2002EP-00011710.  
XX XX  
XX PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
XX PI Heinrich G, Kerb R;  
XX WPI; 2003-342400/32.  
XX DR

XX New use of irinotecan for preparation of pharmaceutical compositions for  
PT treating cancer in subject having genome with variant allele comprising  
PT multidrug resistance 1 polynucleotide.  
XX  
XX Disclosure; SEQ ID NO 664; 104pp; English.  
XX  
CC The invention relates to a novel use of irinotecan or its derivative for  
CC the preparation of a pharmaceutical composition for treating colorectal,  
CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant  
CC glioma in a subject having a genome with a variant allele which comprises  
CC a multidrug resistance 1 (MDR1) polynucleotide. A composition of the  
CC invention has cytostatic activity. The present sequence is used in the  
CC exemplification of the invention.  
XX  
XX Sequence 183610 BP; 50187 A; 43907 C; 42684 G; 45427 T; 0 U; 1405 Other;  
SQ  
Query Match 83.3%; Score 15; DB 10; Length 183610;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGCTTGCTACTGG 15  
Db 107647 ATGCTTGCTACTGG 107633  
RESULT 44  
ACH97379/c  
ID ACH97379 standard; DNA; 192 BP.  
XX  
AC ACH97379;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Klebsiella pneumoniae polynucleotide seqid 3174.  
XX  
KW Recombinant expression vector; transcription regulatory element;  
KW Klebsiella pneumoniae protein; antibacterial; Vaccine; gene; ds.  
XX  
OS Klebsiella pneumoniae.  
XX  
PN US6610836-B1.  
XX  
PD 26-AUG-2003.  
XX  
PF 27-JAN-2000; 2000US-00489039.  
XX  
PR 29-JAN-1999; 99US-0117747P.  
XX  
FA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Breton GL, Osborne M;  
XX  
DR WPI: 2003-895346/82.  
DR P-PSDB; ABO63828.  
XX  
XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for  
PT preparing a vaccine composition against Klebsiella pneumoniae.  
XX  
PS Disclosure; SEQ ID NO 3174; 932pp; English.  
XX  
CC The invention describes a new isolated nucleic acid encoding a Klebsiella  
CC pneumoniae polypeptide. Also described are: a recombinant expression  
CC vector comprising the nucleic acid, operably linked to a transcription  
CC regulatory element; and a cell comprising the recombinant expression  
CC vector. The nucleic acid is useful for preparing a vaccine composition  
CC against Klebsiella pneumoniae. This sequence encodes a Klebsiella  
CC pneumoniae polypeptide of the invention  
XX  
SQ Sequence 192 BP; 46 A; 58 C; 47 G; 41 T; 0 U; 0 Other;  
Query Match 82.2%; Score 14.8; DB 11; Length 192;  
Best Local Similarity 88.9%; Pred. No. 9.3e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 ATGCTTGCTACTGGCTG 18  
Db 43 ATGCTTGCTACTGGCTG 26  
RESULT 45  
ADP57719  
ID ADP57719 standard; cDNA; 225 BP.  
XX  
AC ADP57719;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human polynucleotide sequence SEQ ID NO:86.  
XX  
KW biological activity; genetic engineering; hybridisation probe; oligomer;  
KW primer; chromosome mapping; Gene mapping; recombinant protein production;  
KW human; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2003080795-A2.  
XX  
PD 02-OCT-2003.  
XX  
PF 09-AUG-2002; 2002WO-US025485.  
XX  
PR 09-AUG-2001; 2001US-0311261P.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Yang Y, Wang Z, Weng G, Ma Y;  
XX  
DR WPI: 2003-876918/81.  
DR P-PSDB; ADP58719.  
XX  
PT New polynucleotides, useful as hybridization probes, oligomers or  
PT primers, for chromosome or gene mapping, for the recombinant production  
PT of proteins, and for generating antisense DNA or RNA.  
XX  
PS Claim 1; SEQ ID NO 86; 571pp; English.  
XX  
CC The present sequence represents an isolated polynucleotide sequence (I)  
CC from the present invention, which encodes a polypeptide (II) with  
CC biological activity. Also described: (1) a vector comprising (I); (2) an  
CC expression vector comprising (I); (3) a host cell genetically engineered  
CC to comprise (I) which is operatively associated with a regulatory  
CC sequence that modulates expression of (I) in the host cell; (4) a  
CC polypeptide (II) encoded by (I); (5) a composition comprising the  
CC polypeptide of (4) and a carrier; (6) an antibody directed against the  
CC polypeptide of (4); (7) detecting (I) or the polypeptide of (4) in a  
CC sample; (8) identifying a compound that binds to the polypeptide of (4);  
CC (9) producing the polypeptide of (4); and (10) a collection of  
CC polynucleotides comprising at least one of the polynucleotide sequences  
CC (I). The polynucleotides (I) can be used as hybridisation probes,  
CC oligomers or primers, for chromosome or gene mapping, for the recombinant  
CC production of proteins, and for generating antisense DNA or RNA.  
XX  
SQ Sequence 225 BP; 53 A; 61 C; 67 G; 44 T; 0 U; 0 Other;  
Query Match 82.2%; Score 14.8; DB 10; Length 225;  
Best Local Similarity 88.9%; Pred. No. 9.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 ATGCTTGCTACTGGCTG 18  
Db 190 ATGCTTGCTCCTTGCTG 207  
RESULT 46  
AAH34718/c



Db 204 ATGCTTGCTCCTGGCTG 187

RESULT 48

ABA09266

ID ABA09266 standard; cDNA; 585 BP.

CC ABA09266;

XX 11-JAN-2002 (first entry)

XX Human secreted protein homologue-encoding cDNA, SEQ ID NO:1042.

XX Human; cytokine; cell proliferation; cell differentiation; growth factor;

XX haematopoiesis regulation; tissue growth; immunomodulator; activin;

XX inhibitor; chemotaxis; chemokinesis; thrombolysis; oncogenesis;

XX proliferation; metastasis; cancer; tumour; haematopoietic disorder;

XX myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;

XX chronic inflammatory condition; proliferative retinopathy;

XX atherosclerosis; coronary heart disease; arterial ischaemia;

XX bone disorder; osteoporosis; vascular growth disorder;

XX tissue regeneration; wound healing; infection; immune disorder;

XX cell culture; drug screening; gene therapy; antiinflammatory;

XX antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;

XX cytoskeletal; osteopathic; vasotropic; cardiant; virucide; antibacterial;

XX antifungal; vulvar; antitumor; sa.

XX Homo sapiens.

OS

XX AAS05467

FN WO200157188-A2.

XX 09-AUG-2001.

PD

XX 05-FEB-2001; 2001WO-US003800.

PF

XX 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00360875.

XX (HYSE-) HYSEQ INC.

PA

XX Tang YT, Liu C, Drmanac RT;

PI WPI; 2001-457740/49.

XX P-PSDB; ABB12022.

DR

XX Human proteins and DNA encoding sequences useful for preventing, treating

PT or ameliorating a medical condition in a mammalian subject e.g. arthritis

PT and cancer.

PT

XX Claim 1; Page 873; 1963pp; English.

PS

XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and

CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The

CC invention also relates to vectors and recombinant host cells comprising a

CC nucleotide of the invention, methods of producing the novel polypeptides,

CC antibodies against the polypeptides, methods of detecting the nucleotides

CC or polypeptides in a sample, and methods of identifying compounds which

CC bind to polypeptides of the invention. Although novel, many of the

CC polypeptides of the invention have homology to known proteins, thereby

CC giving an insight into their probable biological activities, and hence

CC potential therapeutic applications. The polypeptides of the invention may

CC have various activities including cytokine, cell proliferation or cell

CC differentiation activities; stem cell growth factor activity;

CC haematopoiesis regulatory activity; tissue growth activity;

CC immunomodulatory activity; activin- or inhibin-related activities;

CC chemotactic or chemokinetic activities; haemostatic, thrombotic or

CC thrombolytic activities; receptor or ligand activities; or may be

CC involved in oncogenesis, cancer cell proliferation or metastasis.

CC Depending on their biological activities, polypeptides and nucleotides of

CC the invention are useful for preventing, treating or ameliorating medical

CC conditions, e.g., by protein or gene therapy. Such conditions include

CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell

CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),

CC

CC proliferative retinopathy, atherosclerosis, coronary heart disease,

CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal

CC vascular growth. Polypeptides involved with tissue regeneration and

CC repair (or nucleic acids encoding them) may be used to promote wound

CC healing (e.g., of burns, incisions and ulcers), while those with

CC immunomodulatory activities may be used in the treatment of viral,

CC bacterial and fungal infections in addition to immune disorders.

CC Polypeptides with growth factor activity may be used in cell cultures to

CC promote cell growth. For example, such polypeptides may be used to

CC manipulate stem cells in culture to give rise to neuroepithelial cells

CC that can be used to augment or replace cells damaged by illness.

CC autoimmune disease or accidental damage. The polypeptides and nucleotides

CC may also be used in the diagnosis of the above conditions, and in drug

CC screening techniques. The present sequence represents a cDNA encoding a

CC novel human polypeptide of the invention

XX

XX Sequence 585 BP; 178 A; 104 C; 108 G; 195 T; 0 U; 0 Other;

QY 1 ATGCTTGCTCCTGGCTG 18

Db 275 AIGCTGGTACGGGCTG 292

RESULT 49

AAS05467

ID AAS05467 standard; DNA; 597 BP.

XX AAS05467;

AC

XX 07-SEP-2001 (first entry)

DT

XX Mammalian vestibular system geotactic behaviour modulator gene #67.

DE

XX Mammalian vestibular system; invertebrate; geotactic behaviour; vertigo;

XX graviperceptive disorder; motion sickness; labyrinthitis; syphilis; ds;

XX Meniere's disease; acoustic neuroma; multiple sclerosis; epilepsy;

XX trauma; infection of the middle ear; ototoxic agent exposure.

XX Drosophila melanogaster.

OS

XX WO200140519-A2.

XX 07-JUN-2001.

PD

XX 01-DEC-2000; 2000WO-US032639.

PF

XX 02-DEC-1999; 99US-0168579P.

PR 26-SEP-2000; 2000US-00669751.

XX (NEUR-) NEUROSCIENCES RES FOUND INC.

XX Greenspan RJ;

XX WPI; 2001-356159/37.

DR

XX New isolated nucleic acid having mammalian vestibular system-modulating

PT activity useful in the treatment of disorders such as motion sickness and

PT vertigo.

PT

XX Claim 59; Page 114; 179pp; English.

PS

XX The sequences shown in AAS05401-AAS05661 represent DNA with mammalian

CC vestibular system-modulating activity. The DNA sequences can be used in a

CC method whereby a first and second strain of an invertebrate is obtained,

CC and both are subjected to conditions in which the strains exhibit

CC different geotactic behaviour. Genes that are differentially expressed in

CC the first strain relative to the second strain are then identified.

CC Mammalian genes having substantially the same nucleic acid sequence as

CC these modulate the mammalian vestibular system. Compounds containing

CC these genes are used to decrease the symptoms of graviorceptive  
 CC disorders such as motion sickness, vertigo, labyrinthitis, Meniere's  
 CC disease, acoustic neuroma, multiple sclerosis, syphilis, trauma,  
 CC infection of the middle ear, exposure to ototoxic agents and epilepsy  
 XX  
 SQ Sequence 597 BP; 171 A; 135 C; 155 G; 136 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 5; Length 597;

Best Local Similarity 88.9%; Pred. No. 1e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ATGCTTGGTACTGGCTG 18  
 ||||| ||||| |||||  
 Db 383 ATGCTTGATCTAGGCTG 400

## RESULT 50

ACF71365

ID ACF71365 standard; DNA; 657 BP.

XX

AC ACF71365;

XX

DT 20-NOV-2003 (first entry)

XX

DE Photorhabdus luminescens nucleotide sequence #9832.

XX

KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;  
 KW detection; food; gene expression; plant; animal; microorganism; toxin;  
 KW antibiotic; biopesticide; virulence factor; disease model; plague;  
 KW whooping cough; Gene; db.

XX

OS Photorhabdus luminescens.

XX

PN WO200294867-A2.

XX

PD 28-NOV-2002.

XX

PF 07-FEB-2002; 2002WO-IB003040.

XX

PR 07-FEB-2001; 2001FR-00001659.

XX

PA (INSP ) INST PASTEUR.

XX

PA (CNRS ) CNRS CENT NAT RECH SCI.

XX

PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;

XX

PI Buchrieser C;

XX

DR WPI; 2003-148459/14.

XX

PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,  
 PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.

XX

PS Claim 2; SEQ ID NO 9832; 1205pp; French.

XX

CC The invention relates to the isolation of genes and their encoded  
 CC proteins from Photorhabdus luminescens. The isolated sequences are  
 CC sources of probes and primers for detecting the genome of P. luminescens  
 CC and related species; to study polymorphisms; for gene analysis and for  
 CC detection/amplification of the genes. Antibodies (Ab) raised against the  
 CC polypeptides encoded by the genes are used for detection/identification  
 CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that  
 CC carry a gene-containing vector are used to select compounds that  
 CC modulate, regulate, induce or inhibit expression of the genes in plants,  
 CC animals or microorganisms other than P. luminescens and are able to alter  
 CC response or sensitivity to toxins and antibiotics produced by P.  
 CC luminescens. Cells transformed to express the genes are useful for  
 CC recombinant production of the proteins, particularly toxins and  
 CC antibacterials useful as insecticides, bactericides and fungicides. The  
 CC genes, proteins, vectors containing the genes and Ab are also useful  
 CC therapeutically to treat microbial infection by bacteria or fungi that  
 CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as  
 CC biopesticides. Other uses of the genes and the proteins are as virulence  
 CC factors and for identifying targets of human diseases for which P.

CC luminescens is a model (particularly plague and whooping cough). This  
 CC sequence represents one of the isolated P. luminescens genes  
 XX

SQ Sequence 657 BP; 169 A; 143 C; 155 G; 190 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 10; Length 657;

Best Local Similarity 88.9%; Pred. No. 1e+03; Mismatches 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ATGCTTGGTACTGGCTG 18

||||| ||||| |||||

Db 376 ATGATGGGTACTGGCTG 393

Search completed: December 3, 2004, 02:26:01

Job time : 295.211 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 2, 2004, 23:31:20 ; Search time 563.921 Seconds  
(without alignments)  
1509.457 Million cell updates/sec

Title: US-10-050-189a-9

Perfect score: 18

Sequence: 1 atgcttggtacttgctg 18

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database :

GenEmbl.\*

1: gb\_pa.\*

2: gb\_hgt.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6	AX481362 Sequence
2	18	100.0	66479	6	AX676048 Sequence
3	18	100.0	78376	9	AL359692 Human DNA
4	17	94.4	44415	2	AC119879 Mus muscu
5	17	94.4	146632	2	AC115935 Mus muscu
6	17	94.4	164176	2	AC116409 Mus muscu
7	17	94.4	296100	1	AP005086 Vibrio pa
8	16.4	91.1	476	11	HS606D23T
9	16.4	91.1	1122	6	AR320510 Sequence
10	16.4	91.1	1923	1	AF355751
11	16.4	91.1	2100	5	AY189696 Bacthrops
12	16.4	91.1	2735	5	BC060419 Xenopus 1
13	16.4	91.1	13629	6	C0578918 Sequence
14	16.4	91.1	17997	2	AC019883 Drosophil
15	16.4	91.1	51794	9	AL845315 Human DNA
16	16.4	91.1	58294	2	AL213988 Homo sapi
17	16.4	91.1	70663	2	AC073400 Homo sapi
18	16.4	91.1	74377	9	AC010499 Homo sapi
19	16.4	91.1	93330	2	AC022591 Homo sapi

C	20	16.4	91.1	93375	3	AC005554
C	21	16.4	91.1	93338	9	AC024567
C	22	16.4	91.1	101456	9	AF188026 Homo sapi
C	23	16.4	91.1	101459	9	AC090776 Homo sapi
C	24	16.4	91.1	125145	2	AC022136 Homo sapi
C	25	16.4	91.1	135427	10	AC101834
C	26	16.4	91.1	142071	2	AC149958
C	27	16.4	91.1	149561	10	AL808021
C	28	16.4	91.1	156842	2	AC064820
C	29	16.4	91.1	164920	3	AC092187
C	30	16.4	91.1	170740	9	HSBA80K6
C	31	16.4	91.1	178597	9	AL215000
C	32	16.4	91.1	182955	9	AL445237
C	33	16.4	91.1	184554	3	AC099022
C	34	16.4	91.1	186298	9	AC007860
C	35	16.4	91.1	186314	2	AC021071
C	36	16.4	91.1	193985	2	AC122284
C	37	16.4	91.1	193450	9	AC005674
C	38	16.4	91.1	211919	10	AC117260
C	39	16.4	91.1	220483	2	AC110865
C	40	16.4	91.1	242533	10	AC140455
C	41	16.4	91.1	244291	2	AC107416
C	42	16.4	91.1	252813	2	AC118528
C	43	16.4	91.1	262126	2	AC098502
C	44	16.4	91.1	282122	2	AC120474
C	45	16.4	91.1	314957	3	AE003581
C	46	16.4	91.1	345829	1	BS571868
C	47	16.4	91.1	349980	6	AX770905
C	48	16	88.9	105866	2	AC021602
C	49	16	88.9	148540	9	HS21299
C	50	16	88.9	157256	5	AL933064
C	51	16	88.9	159445	8	AL114474
C	52	16	88.9	167335	2	AC023527
C	53	16	88.9	177744	2	BS666060
C	54	16	88.9	177876	10	AC133093
C	55	16	88.9	182798	2	AC120604
C	56	16	88.9	192267	8	AC092748
C	57	16	88.9	228573	2	AC134941
C	58	16	88.9	234515	2	AC098639
C	59	16	88.9	243487	2	AC094582
C	60	16	88.9	253419	2	AC111634
C	61	16	88.9	272630	2	AC094183
C	62	16	88.9	303332	8	AE017087
C	63	15.4	85.6	511	3	AY462649
C	64	15.4	85.6	525	9	HUMYR23E03
C	65	15.4	85.6	530	3	AY462648
C	66	15.4	85.6	745	5	CR385711
C	67	15.4	85.6	787	8	AF014051
C	68	15.4	85.6	1074	6	CQ649538
C	69	15.4	85.6	1533	8	AK073298
C	70	15.4	85.6	2009	8	AK107048
C	71	15.4	85.6	2124	5	BC074555
C	72	15.4	85.6	2794	8	SCYOR364W
C	73	15.4	85.6	3209	10	AF539744
C	74	15.4	85.6	10283	1	AE006528
C	75	15.4	85.6	10607	1	AE010013
C	76	15.4	85.6	13754	10	AF367475
C	77	15.4	85.6	15382	9	AF222689
C	78	15.4	85.6	18234	14	AF017149
C	79	15.4	85.6	22004	2	AC017362
C	80	15.4	85.6	34721	9	HS315G5
C	81	15.4	85.6	38093	8	AF487263
C	82	15.4	85.6	47481	2	AC011874
C	83	15.4	85.6	49197	8	AP006349
C	84	15.4	85.6	51719	1	AE014147
C	85	15.4	85.6	51046	2	AL356970
C	86	15.4	85.6	57144	2	AC100329
C	87	15.4	85.6	60268	9	AC016876
C	88	15.4	85.6	61884	9	HSDJ235B9
C	89	15.4	85.6	65145	2	AC024310
C	90	15.4	85.6	75877	9	AP005401
C	91	15.4	85.6	78386	2	AC015466
C	92	15.4	85.6	81975	2	AC005415

AC005554	Drosophil
AC024567	Homo sapi
AF188026	Homo sapi
AC090776	Homo sapi
AC022136	Homo sapi
AC101834	Mus muscu
AC149958	Strongylo
AL808021	Mouse DNA
AC064820	Homo sapi
AC092187	Drosophil
AL121502	Human DNA
AC125000	Mus muscu
AL445237	Human DNA
AC099022	Drosophil
AC007860	Homo sapi
AC021071	Homo sapi
AC122284	Mus muscu
AC005674	Homo sapi
AC117260	Mus muscu
AC110865	Rattus no
AC140455	Mus muscu
AC107416	Rattus no
AC118528	Rattus no
AC098502	Rattus no
AC120474	Rattus no
AE003581	Drosophil
BS571868	Phototrab
AX770905	Sequence
AC021602	Homo sapi
AC133093	Mus muscu
AC120604	Rattus no
AC092748	Genomic s
AC134941	Rattus no
AC098639	Rattus no
AC094582	Rattus no
AC111634	Rattus no
AC094183	Rattus no
AE017087	Oryza sat
AY462649	Plasmodiu
AF085918	Homo sapi
AY462648	Plasmodiu
CR385711	Gallus ga
AF014051	Nicotiana
CQ649538	Sequence
AK073298	Oryza sat
AK107048	Oryza sat
BC074555	Xenopus t
Z75272	S.cerevisia
AF539744	Mus muscu
AE006528	Streptoco
AE010013	Streptoco
AF367475	Mus muscu
AF222689	Homo sapi
AF017149	Hendra vi
AC017362	Drosophil
AL031708	Human DNA
AF487263	Leptospha
AC011874	Homo sapi
AP006349	Lotus cor
AE014147	Streptoco
AL356970	Human DNA
AC100329	Mus muscu
AC016876	Homo sapi
AL121941	Human DNA
AC024310	Homo sapi
AP005401	Homo sapi
AC015466	Homo sapi
AC005415	Drosophil

C 93	15.4	85.6	83039	9	AL137074	AL137074 Human DNA	C 166	15.4	85.6	172307	2	AC044842	AC044842 Homo sapi
C 94	15.4	85.6	84334	8	AB010698	AB010698 Arabidops	C 167	15.4	85.6	172521	2	AC013582	AC013582 Homo sapi
C 95	15.4	85.6	87616	2	AL133540	AL133540 Homo sapi	C 168	15.4	85.6	172663	2	AC107839	AC107839 Mus muscu
C 96	15.4	85.6	88318	8	AF002842	AF002842 Oryza sat	C 169	15.4	85.6	172837	9	AL450304	AL450304 Human DNA
C 97	15.4	85.6	89452	9	AC005246	AC005246 Homo sapi	C 170	15.4	85.6	172883	9	AP003967	AP003967 Homo sapi
C 98	15.4	85.6	92837	2	AC005716	AC005716 Drosophil	C 171	15.4	85.6	172918	2	AC148306	AC148306 Pan trogl
C 99	15.4	85.6	95603	8	AP003543	AP003543 Oryza sat	C 172	15.4	85.6	172918	2	AC148306	AC148306 Pan trogl
C 100	15.4	85.6	98190	2	AC125738	Continuation (4 of	C 173	15.4	85.6	173422	2	AC127438	AC127438 Rattus no
C 101	15.4	85.6	98392	2	AL590620	AL590620 Homo sapi	C 174	15.4	85.6	173553	2	AC102837	AC102837 Mus muscu
C 102	15.4	85.6	103485	9	HUAC002301	AC002301 Homo sapi	C 175	15.4	85.6	174007	9	AC023831	AC023831 Homo sapi
C 103	15.4	85.6	110000	1	CP000003_05	Continuation (6 of	C 176	15.4	85.6	174363	9	AC009133	AC009133 Homo sapi
C 104	15.4	85.6	110000	1	CP000003_06	Continuation (7 of	C 177	15.4	85.6	175007	3	AC008342	AC008342 Drosophil
C 105	15.4	85.6	110000	2	AC091341_1	Continuation (2 of	C 178	15.4	85.6	175007	3	AC008342	AC008342 Drosophil
C 106	15.4	85.6	110000	2	AC095360_1	Continuation (2 of	C 179	15.4	85.6	175425	2	AC020918	AC020918 Homo sapi
C 107	15.4	85.6	110000	2	AC095360_2	Continuation (3 of	C 180	15.4	85.6	175493	2	AC020769	AC020769 Homo sapi
C 108	15.4	85.6	110000	2	AC119867_1	Continuation (3 of	C 181	15.4	85.6	175643	2	AC018780	AC018780 Homo sapi
C 109	15.4	85.6	110000	2	AC125738_1	Continuation (2 of	C 182	15.4	85.6	176762	2	AC141309	AC141309 Homo sapi
C 110	15.4	85.6	110000	2	AC148613_2	Continuation (3 of	C 183	15.4	85.6	177432	2	AC118274	AC118274 Homo sapi
C 111	15.4	85.6	111431	5	AL954694	AL954694 Zebrafish	C 184	15.4	85.6	177512	2	AC139330	AC139330 Mus muscu
C 112	15.4	85.6	112414	6	BD143114	BD143114 DNA encod	C 185	15.4	85.6	177792	9	CNS06C7M	AL390254 Human chr
C 113	15.4	85.6	117345	9	AP001775	AP001775 Homo sapi	C 186	15.4	85.6	178931	2	AC143039	AC143039 Macaca mu
C 114	15.4	85.6	117602	2	AC087055	AC087055 Homo sapi	C 187	15.4	85.6	179453	10	AC119893	AC119893 Mus muscu
C 115	15.4	85.6	121228	8	CNS07YFV	AL731761 Oryza sat	C 188	15.4	85.6	180645	10	AC115883	AC115883 Mus muscu
C 116	15.4	85.6	121476	6	CO815032	CO815032 Sequence	C 189	15.4	85.6	180946	3	AC007827	AC007827 Drosophil
C 117	15.4	85.6	128757	9	AL359837	AL359837 Human DNA	C 190	15.4	85.6	182109	2	AC140817	AC140817 Homo sapi
C 118	15.4	85.6	132449	9	AL365272	AL365272 Human DNA	C 191	15.4	85.6	182925	2	AC128749	AC128749 Rattus no
C 119	15.4	85.6	136856	9	AL354654	AL354654 Human DNA	C 192	15.4	85.6	183099	2	AC117349	AC117349 Rattus no
C 120	15.4	85.6	137824	2	AC146827	AC146827 Carollia	C 193	15.4	85.6	183972	10	AC117223	AC117223 Mus muscu
C 121	15.4	85.6	139226	9	AC008650	AC008650 Homo sapi	C 194	15.4	85.6	184133	2	AC135898	AC135898 Rattus no
C 122	15.4	85.6	139760	2	CR388023	CR388023 Danio rer	C 195	15.4	85.6	184254	9	AC131935	AC131935 Homo sapi
C 123	15.4	85.6	139946	8	AC118133	AC118133 Oryza sat	C 196	15.4	85.6	184737	2	AC124566	AC124566 Mus muscu
C 124	15.4	85.6	141130	9	AC084208	AC084208 Homo sapi	C 197	15.4	85.6	184737	2	AC124566	AC124566 Mus muscu
C 125	15.4	85.6	141877	10	AC069836	AC069836 Mouse DNA	C 198	15.4	85.6	185876	2	AC133266	AC133266 Rattus no
C 126	15.4	85.6	143687	9	AC016572	AC016572 Homo sapi	C 199	15.4	85.6	186303	5	EX004974	EX004974 Zebrafish
C 127	15.4	85.6	146836	9	AC019317	AC019317 Homo sapi	C 200	15.4	85.6	187235	2	AP001785	AP001785 Homo sapi
C 128	15.4	85.6	146850	2	AC141349	AC141349 Rattus no	C 201	15.4	85.6	187543	2	AC141261	AC141261 Homo sapi
C 129	15.4	85.6	148371	9	AC1417061	AC1417061 Pan trogl	C 202	15.4	85.6	188044	2	AC128753	AC128753 Rattus no
C 130	15.4	85.6	149202	2	AC022160	AC022160 Homo sapi	C 203	15.4	85.6	188666	2	AC108921	AC108921 Homo sapi
C 131	15.4	85.6	149310	2	AC148196	AC148196 Callithri	C 204	15.4	85.6	188716	5	AL807739	AL807739 Zebrafish
C 132	15.4	85.6	149562	3	AB159446	AB159446 Bombyx mo	C 205	15.4	85.6	188920	2	AC140709	AC140709 Homo sapi
C 133	15.4	85.6	152698	2	AC140802	AC140802 Mus muscu	C 206	15.4	85.6	189055	9	AC015724	AC015724 Homo sapi
C 134	15.4	85.6	154323	2	AC025831	AC025831 Homo sapi	C 207	15.4	85.6	189785	2	AC115727	AC115727 Mus muscu
C 135	15.4	85.6	154414	9	HS900224	AL008723 Human DNA	C 208	15.4	85.6	190453	2	AC139253	AC139253 Homo sapi
C 136	15.4	85.6	154764	8	AP005523	AP005523 Oryza sat	C 209	15.4	85.6	190455	2	AC141295	AC141295 Homo sapi
C 137	15.4	85.6	155106	8	AP017988	AP017988 Oryza sat	C 210	15.4	85.6	194254	2	AC112264	AC112264 Mus muscu
C 138	15.4	85.6	155317	9	AC145336	AC145336 Homo sapi	C 211	15.4	85.6	194304	9	AC016708	AC016708 Homo sapi
C 139	15.4	85.6	157417	9	AC097378	AC097378 Homo sapi	C 212	15.4	85.6	195358	2	AC040892	AC040892 Homo sapi
C 140	15.4	85.6	158111	2	AC121548	AC121548 Homo sapi	C 213	15.4	85.6	195863	2	AC118572	AC118572 Lemur cat
C 141	15.4	85.6	158368	2	AC139466	AC139466 Mus muscu	C 214	15.4	85.6	196247	4	AC150696	AC150696 Bos tauru
C 142	15.4	85.6	158368	2	AC139466	AC139466 Homo sapi	C 215	15.4	85.6	196378	2	AC140958	AC140958 Didelphis
C 143	15.4	85.6	159463	3	AP011668	AP011668 Rattus no	C 216	15.4	85.6	196441	2	AC121495	AC121495 Mus muscu
C 144	15.4	85.6	159598	9	AP004386	AP004386 Homo sapi	C 217	15.4	85.6	196715	2	AC141600	AC141600 Homo sapi
C 145	15.4	85.6	159661	8	AY387483	AY387483 Oryza sat	C 218	15.4	85.6	196835	2	AC142538	AC142538 Homo sapi
C 146	15.4	85.6	159752	2	AC114241	AC114241 Rattus no	C 219	15.4	85.6	196840	2	AC023255	AC023255 Homo sapi
C 147	15.4	85.6	160161	2	AC147453	AC147453 Carollia	C 220	15.4	85.6	196928	2	AP000847	AP000847 Homo sapi
C 148	15.4	85.6	161582	2	AC026028	AC026028 Homo sapi	C 221	15.4	85.6	197877	9	AC090142	AC090142 Homo sapi
C 149	15.4	85.6	164198	2	AC016801	AC016801 Homo sapi	C 222	15.4	85.6	197926	2	AC010550	AC010550 Homo sapi
C 150	15.4	85.6	164201	9	AL157935	AL157935 Human DNA	C 223	15.4	85.6	198176	2	AC063127	AC063127 Homo sapi
C 151	15.4	85.6	166525	9	AC022413	AC022413 Homo sapi	C 224	15.4	85.6	198255	9	AC005090	AC005090 Homo sapi
C 152	15.4	85.6	167081	2	AC121565	AC121565 Mus muscu	C 225	15.4	85.6	200288	2	AC119725	AC119725 Homo sapi
C 153	15.4	85.6	168197	9	AC023307	AC023307 Homo sapi	C 226	15.4	85.6	200853	9	CNS01DSQ	AL121839 Human chr
C 154	15.4	85.6	168418	9	AC009403	AC009403 Homo sapi	C 227	15.4	85.6	203073	10	AC146815	AC146815 Mus muscu
C 155	15.4	85.6	168692	2	AL136986	AL136986 Homo sapi	C 228	15.4	85.6	204001	9	AC087783	AC087783 Mouse sapi
C 156	15.4	85.6	168862	9	AC022024	AC022024 Homo sapi	C 229	15.4	85.6	204136	10	AL772271	AL772271 Mouse DNA
C 157	15.4	85.6	169478	2	AC139280	AC139280 Homo sapi	C 230	15.4	85.6	204407	2	AC021446	AC021446 Mus muscu
C 158	15.4	85.6	169841	2	AC099793	AC099793 Homo sapi	C 231	15.4	85.6	204480	2	AC015083	AC015083 Homo sapi
C 159	15.4	85.6	170044	2	AC116796	AC116796 Mus muscu	C 232	15.4	85.6	204682	2	AC135020	AC135020 Rattus no
C 160	15.4	85.6	170284	9	AL359739	AL359739 Human DNA	C 233	15.4	85.6	206252	2	AC141064	AC141064 Homo sapi
C 161	15.4	85.6	170703	10	AC125111	AC125111 Mus muscu	C 234	15.4	85.6	206560	2	AC139514	AC139514 Rattus no
C 162	15.4	85.6	170979	9	AC007950	AC007950 Homo sapi	C 235	15.4	85.6	206843	2	AC099605	AC099605 Mus muscu
C 163	15.4	85.6	171065	2	AC132599	AC132599 Mus muscu	C 236	15.4	85.6	207436	2	AC140823	AC140823 Homo sapi
C 164	15.4	85.6	171099	2	AC135249	AC135249 Rattus no	C 237	15.4	85.6	208470	10	AL928883	AL928883 Mouse DNA
C 165	15.4	85.6	171456	9	AC032591	AC032591 Homo sapi	C 238	15.4	85.6	209120	2	AC095998	AC095998 Rattus no
C 166	15.4	85.6	171596	9	AC139750	AC139750 Homo sapi	C 239	15.4	85.6	209215	10	AL732311	AL732311 Mouse DNA

239	15.4	85.6	209844	9	AC011495	AC011495 Homo sapi	312	15	83.3	1712	8	AK073122	Oryza sat
240	15.4	85.6	211381	10	AC116404	AC116404 Mus muscu	c 313	15	83.3	2166	3	BT001304	Drosophil
241	15.4	85.6	211552	2	AC141271	AC141271 Homo sapi	314	15	83.3	2418	6	AX879282	Sequence
242	15.4	85.6	211784	2	AC017903	AC017903 Drosophil	315	15	83.3	2418	6	BD157753	Primer fo
243	15.4	85.6	214979	4	AC147680	AC147680 Canis Fam	316	15	83.3	2418	9	AK022529	Homo sapi
244	15.4	85.6	216289	2	AC123712	AC123712 Mus muscu	317	15	83.3	2975	9	BC035115	Homo sapi
245	15.4	85.6	217521	9	AC023825	AC023825 Homo sapi	318	15	83.3	3710	9	HSM807632	Homo sapi
246	15.4	85.6	217614	2	AC137754	AC137754 Mus muscu	319	15	83.3	4265	6	CO914558	Sequence
247	15.4	85.6	217960	2	AC128963	AC128963 Rattus no	320	15	83.3	4584	6	CO497444	Sequence
248	15.4	85.6	218008	2	AC139438	AC139438 Rattus no	321	15	83.3	5170	6	CO412492	Sequence
249	15.4	85.6	218485	2	AC127470	AC127470 Pan trogl	322	15	83.3	5415	6	BD183319	Novel gen
250	15.4	85.6	219181	2	AC141063	AC141063 Homo sapi	323	15	83.3	7120	6	CO576203	Sequence
251	15.4	85.6	219704	10	AL772181	AL772181 Mouse DNA	324	15	83.3	7984	9	AF304448	Homo sapi
252	15.4	85.6	220212	2	AC141603	AC141603 Homo sapi	325	15	83.3	7984	9	AF304448	Homo sapi
253	15.4	85.6	221898	10	AL669891	AL669891 Mouse DNA	326	15	83.3	7984	9	AF304448	Homo sapi
254	15.4	85.6	221982	2	AC094396	AC094396 Rattus no	327	15	83.3	12952	1	AE014882	Streptoco
255	15.4	85.6	223843	10	AC102595	AC102595 Mus muscu	328	15	83.3	15666	1	AE004345	Vibrio ch
256	15.4	85.6	225702	10	AC123718	AC123718 Mus muscu	329	15	83.3	17155	1	AE273169	Rhodobact
257	15.4	85.6	225702	10	AL626768	AL626768 Mouse DNA	330	15	83.3	37221	2	AC013974	Drosophil
258	15.4	85.6	227165	2	AC123473	AC123473 Rattus no	331	15	83.3	71179	9	AL136110	Human DNA
259	15.4	85.6	228182	2	AC115828	AC115828 Mus muscu	332	15	83.3	83321	2	AC013960	Drosophil
260	15.4	85.6	228405	2	AC123473	AC123473 Rattus no	333	15	83.3	103244	3	AC090524	Caenorhab
261	15.4	85.6	228634	2	AC096145	AC096145 Rattus no	334	15	83.3	103563	10	AL929313	Mouse DNA
262	15.4	85.6	228902	2	AC098116	AC098116 Rattus no	335	15	83.3	110000	2	AC094316	Rattus no
263	15.4	85.6	231166	2	AC134074	AC134074 Rattus no	336	15	83.3	115625	9	AC093029	Homo sapi
264	15.4	85.6	231406	2	AC126073	AC126073 Rattus no	337	15	83.3	118635	8	AP005862	Oryza sat
265	15.4	85.6	231484	2	AC096379	AC096379 Rattus no	338	15	83.3	119945	9	HS218J18	Human DNA
266	15.4	85.6	232302	3	AE003766	AE003766 Drosophil	339	15	83.3	131611	9	AC005099	Homo sapi
267	15.4	85.6	233499	10	AC110236	AC110236 Mus muscu	340	15	83.3	140952	2	AC079982	Homo sapi
268	15.4	85.6	234122	2	AC137172	AC137172 Rattus no	341	15	83.3	145380	9	AL357129	Human DNA
269	15.4	85.6	235551	2	AC130518	AC130518 Rattus no	342	15	83.3	147210	9	AC008391	Homo sapi
270	15.4	85.6	237222	2	AC121742	AC121742 Rattus no	343	15	83.3	149146	2	AL583851	Homo sapi
271	15.4	85.6	237985	2	AC113789	AC113789 Rattus no	344	15	83.3	152614	2	AC044881	Homo sapi
272	15.4	85.6	239069	2	AC108289	AC108289 Rattus no	345	15	83.3	153899	10	AL772285	Mouse DNA
273	15.4	85.6	241510	2	AC094856	AC094856 Rattus no	346	15	83.3	154090	2	AC142024	Rattus no
274	15.4	85.6	242324	10	AC093478	AC093478 Mus muscu	347	15	83.3	155584	2	AC103399	Mus muscu
275	15.4	85.6	242384	2	AC105847	AC105847 Rattus no	348	15	83.3	161643	2	AC139200	Mus muscu
276	15.4	85.6	246248	2	AC108047	AC108047 Rattus no	349	15	83.3	162188	10	EX000537	Mouse DNA
277	15.4	85.6	249413	2	AC095008	AC095008 Rattus no	350	15	83.3	162488	2	AC022184	Homo sapi
278	15.4	85.6	250322	2	AC097695	AC097695 Rattus no	351	15	83.3	166247	2	AC135876	Rattus no
279	15.4	85.6	251412	2	AC136586	AC136586 Rattus no	352	15	83.3	169624	2	AC118618	Mus muscu
280	15.4	85.6	253798	2	AC129701	AC129701 Rattus no	353	15	83.3	173071	9	AC009477	Homo sapi
281	15.4	85.6	255652	3	AE003811	AE003811 Drosophil	354	15	83.3	173254	10	AL732396	Mouse DNA
282	15.4	85.6	256059	2	AC098893	AC098893 Rattus no	355	15	83.3	173698	9	AC022431	Homo sapi
283	15.4	85.6	259889	2	AC125704	AC125704 Rattus no	356	15	83.3	173738	2	AC147314	Pan trogl
284	15.4	85.6	260905	2	AC135480	AC135480 Rattus no	357	15	83.3	173738	2	AC147314	Pan trogl
285	15.4	85.6	261688	2	AC111685	AC111685 Rattus no	358	15	83.3	173927	3	AC009538	Drosophil
286	15.4	85.6	261847	2	AC130670	AC130670 Mus muscu	359	15	83.3	176871	10	AC124687	Mus muscu
287	15.4	85.6	262883	2	AC109389	AC109389 Rattus no	360	15	83.3	177441	2	AC100500	Mus muscu
288	15.4	85.6	263505	10	AC139673	AC139673 Mus muscu	361	15	83.3	177909	2	AC031997	Homo sapi
289	15.4	85.6	266884	2	AC115547	AC115547 Rattus no	362	15	83.3	183407	2	AC021572	Homo sapi
290	15.4	85.6	268844	2	AC108564	AC108564 Rattus no	363	15	83.3	183610	2	AC026452	Homo sapi
291	15.4	85.6	270150	9	AE006639	AE006639 Homo sapi	364	15	83.3	183610	6	AX706966	Sequence
292	15.4	85.6	271546	3	AE014843	AE014843 Plasmodiu	365	15	83.3	187361	2	AC112957	Sequence
293	15.4	85.6	272866	2	AC134363	AC134363 Rattus no	366	15	83.3	189049	9	AC008667	Homo sapi
294	15.4	85.6	276412	2	AC113494	AC113494 Mus muscu	367	15	83.3	190672	3	AC008357	Drosophil
295	15.4	85.6	279877	2	AC113289	AC113289 Mus muscu	368	15	83.3	195653	2	AC108127	Homo sapi
296	15.4	85.6	286363	1	AP005077	AP005077 Rattus no	369	15	83.3	200741	10	AC110819	Mus muscu
297	15.4	85.6	299130	2	AC095687	AC095687 Rattus no	370	15	83.3	201070	2	AC026291	Homo sapi
298	15.4	85.6	313378	2	AC094420	AC094420 Rattus no	371	15	83.3	201493	9	AL691520	Human DNA
299	15.4	85.6	325493	2	AC107171	AC107171 Rattus no	372	15	83.3	201493	2	AC135863	Mus muscu
300	15.4	85.6	325650	1	AP005145	AP005145 Streptoco	373	15	83.3	207383	2	AC116673	Mus muscu
301	15.4	85.6	330919	1	AP005296	AP005296 Rattus no	374	15	83.3	207383	2	AC109112	Rattus no
302	15.4	85.6	333550	1	AP003593	AP003593 Nostoc sp	375	15	83.3	207418	9	AC148447	Pan trogl
303	15.4	85.6	348505	1	EX571870	EX571870 Photorhab	376	15	83.3	21047	2	AL645475	Homo sapi
304	15.4	85.6	349980	6	AX770909	AX770909 Sequence	377	15	83.3	213393	2	AL645475	Homo sapi
305	15.4	85.6	349981	6	AX647880	AX647880 Sequence	378	15	83.3	213393	2	AL645475	Homo sapi
306	15.4	85.6	357	6	CO657467	CO657467 Sequence	379	15	83.3	215401	10	AC136926	Mus muscu
307	15.4	85.6	740	6	BD020471	BD020471 Novel gen	380	15	83.3	215494	2	AC138300	Mus muscu
308	15.4	85.6	740	6	BD100409	BD100409 Novel gen	381	15	83.3	223266	2	AC114422	Rattus no
309	15.4	85.6	884	6	AX867105	AX867105 Sequence	382	15	83.3	224517	2	AC098602	Rattus no
310	15.4	85.6	1116	6	BD147167	BD147167 Primer fo	383	15	83.3	225063	2	AC135293	Mus muscu
311	15.4	85.6	1683	10	BC031458	BC031458 Mus muscu	384	15	83.3	225136	2	AC095251	Rattus no
							c 384	15	83.3	227557	2	AC127732	Rattus no

385	15	83.3	228329	2	AC034098	AC034098 Mus muscu	458	14.8	82.2	3	AB003329	AB003329 Leishmani
386	15	83.3	228597	2	AC107556	AC107556 Rattus no	C 459	14.8	82.2	3	AB107302	AB107302 Drosophil
387	15	83.3	232188	10	AL672055	Mouse DNA	C 460	14.8	82.2	3	AB107282	AB107282 Drosophil
388	15	83.3	237308	2	AC009593	Homo sapi	C 461	14.8	82.2	4665	AB089438	AB089438 Streptoco
389	15	83.3	239442	2	AC118635	Mus muscu	C 462	14.8	82.2	5348	CQ573809	CQ573809 Sequence
390	15	83.3	240200	2	AC122075	Rattus no	C 463	14.8	82.2	5551	AF112114	AF112114 Mus muscu
391	15	83.3	244545	2	AC118385	Rattus no	C 464	14.8	82.2	5884	CQ608249	CQ608249 Sequence
392	15	83.3	245581	10	AC133000	AC133000 Rattus no	C 465	14.8	82.2	6196	CQ599594	CQ599594 Sequence
393	15	83.3	250865	2	AC094899	AC094899 Rattus no	C 466	14.8	82.2	7763	MINCND	MINCND
394	15	83.3	254650	1	AP005347	Vibrio vu	C 467	14.8	82.2	11326	AC017527	AC017527 Drosophil
395	15	83.3	260168	3	AC003687	Drosophil	C 468	14.8	82.2	12344	AE0009787	AE0009787 Pyrobacul
396	15	83.3	260224	2	AC130084	Rattus no	C 469	14.8	82.2	13148	AE0009891	AE0009891 Pyrobacul
397	15	83.3	263436	2	AC139055	AC139055 Mus muscu	C 470	14.8	82.2	14148	BX548014	BX548014 Mouse DNA
398	15	83.3	270962	2	AC139674	AC139674 Mus muscu	C 471	14.8	82.2	14820	AC012988	AC012988 Drosophil
399	15	83.3	296091	3	AE003602	AE003602 Drosophil	C 472	14.8	82.2	16124	AC017158	AC017158 Drosophil
400	15	83.3	317209	2	AL772175	Mus muscu	C 473	14.8	82.2	20503	AL359534	AL359534 Human DNA
401	14.8	82.2	192	6	AB386445	AB386445 Sequence	C 474	14.8	82.2	21229	AC015141	AC015141 Drosophil
402	14.8	82.2	310	6	CQ660846	CQ660846 Sequence	C 475	14.8	82.2	24103	CC382131	CC382131-42
403	14.8	82.2	382	11	BV092096	REPAMSEQ0	C 476	14.8	82.2	26677	SCCVIIRA	SCCVIIRA
404	14.8	82.2	398	6	CQ661178	CQ661178 Sequence	C 477	14.8	82.2	30175	AC008291	AC008291 Drosophil
405	14.8	82.2	445	11	BV017126	BV017126 S212P6363	C 478	14.8	82.2	30696	AC004778	AC004778 Homo sapi
406	14.8	82.2	456	6	CQ697058	CQ697058 Sequence	C 479	14.8	82.2	30889	CQ599261	CQ599261 Sequence
407	14.8	82.2	478	11	G50065	SHGC-82922	C 480	14.8	82.2	31563	CQ573590	CQ573590 Sequence
408	14.8	82.2	499	8	HVU234424	HVU234424 Hordeum v	C 481	14.8	82.2	32000	SPBC577	SPBC577
409	14.8	82.2	597	6	AX154718	AX154718 Sequence	C 482	14.8	82.2	33327	AC114953	AC114953 Homo sapi
410	14.8	82.2	598	11	BV042427	BV042427 S212P6038	C 483	14.8	82.2	34639	AC005765	AC005765 Homo sapi
411	14.8	82.2	599	11	BV004450	BV004450 S209P6182	C 484	14.8	82.2	34683	HSU09822	HSU09822 Human cosm
412	14.8	82.2	599	11	BV004450	BV004450 S209P6182	C 485	14.8	82.2	34882	AC014444	AC014444 Drosophil
413	14.8	82.2	646	11	BV066383	BV066383 S212P6756	C 486	14.8	82.2	38116	AL445287	AL445287 Human DNA
414	14.8	82.2	650	11	BV019315	BV019315 S212P6011	C 487	14.8	82.2	38189	CQ599267	CQ599267 Sequence
415	14.8	82.2	664	9	HS4336722	HS4336722 Homo sapi	C 488	14.8	82.2	39814	CQ599264	CQ599264 Sequence
416	14.8	82.2	681	6	CQ597024	CQ597024 Sequence	C 489	14.8	82.2	39872	HSICB2046	HSICB2046
417	14.8	82.2	710	11	BV043754	BV043754 S212P6679	C 490	14.8	82.2	40419	AC004653	AC004653 Homo sapi
418	14.8	82.2	847	6	CQ587559	CQ587559 Sequence	C 491	14.8	82.2	45298	AC005404	AC005404 Homo sapi
419	14.8	82.2	887	3	AY069202	AY069202 Drosophil	C 492	14.8	82.2	47310	AX059549	AX059549 Sequence
420	14.8	82.2	1012	10	BC013538	BC013538 Mus muscu	C 493	14.8	82.2	48267	AC018238	AC018238 Drosophil
421	14.8	82.2	1242	6	AR376857	AR376857 Sequence	C 494	14.8	82.2	50955	AC017953	AC017953 Drosophil
422	14.8	82.2	1424	5	BX929542	BX929542 Gallus ga	C 495	14.8	82.2	52115	AC140598	AC140598 Macaca mu
423	14.8	82.2	1463	6	AX130430	AX130430 Homo sapi	C 496	14.8	82.2	53067	AC100275	AC100275 Mus muscu
424	14.8	82.2	1467	6	AR447884	AR447884 Sequence	C 497	14.8	82.2	53423	AL591419	AL591419 Human DNA
425	14.8	82.2	1475	10	BC057963	BC057963 Mus muscu	C 498	14.8	82.2	54194	AL162453	AL162453 Human DNA
426	14.8	82.2	1551	5	BX935173	BX935173 Gallus ga	C 499	14.8	82.2	54388	AC015233	AC015233 Drosophil
427	14.8	82.2	1610	5	CR524131	CR524131 Gallus ga	C 500	14.8	82.2	57000	AC078862	AC078862 Homo sapi
428	14.8	82.2	1638	6	AX512998	AX512998 Sequence	C 501	14.8	82.2	57507	AL603652	AL603652 Human DNA
429	14.8	82.2	1651	5	CH523527	CH523527 Gallus ga	C 502	14.8	82.2	57550	AC100408	AC100408 Mus muscu
430	14.8	82.2	1762	9	AX093649	AX093649 Homo sapi	C 503	14.8	82.2	58414	Continuation (5 of	Continuation (5 of
431	14.8	82.2	1786	3	AF171859	AF171859 Drosophil	C 504	14.8	82.2	60169	AL596257	AL596257 Human DNA
432	14.8	82.2	1991	4	AY522920	AY522920 Sus scrof	C 505	14.8	82.2	60657	AC101392	AC101392 Mus muscu
433	14.8	82.2	2019	10	BC063758	BC063758 Mus muscu	C 506	14.8	82.2	61031	AC110581	AC110581 Homo sapi
434	14.8	82.2	2094	6	AR451017	AR451017 Sequence	C 507	14.8	82.2	61031	AC110581	AC110581 Homo sapi
435	14.8	82.2	2134	10	BC066042	BC066042 Mus muscu	C 508	14.8	82.2	61373	AC115997	AC115997 Homo sapi
436	14.8	82.2	2244	9	AK121994	AK121994 Homo sapi	C 509	14.8	82.2	63292	FL4G16	FL4G16 Arabidops
437	14.8	82.2	2338	9	HS4515384	HS4515384 Homo sapi	C 510	14.8	82.2	63416	AC136323	AC136323 Homo sapi
438	14.8	82.2	2449	6	AX523744	AX523744 Sequence	C 511	14.8	82.2	63923	AC008292	AC008292 Drosophil
439	14.8	82.2	2453	6	AX523716	AX523716 Sequence	C 512	14.8	82.2	64011	AC007642	AC007642 Homo sapi
440	14.8	82.2	2463	6	AX523762	AX523762 Sequence	C 513	14.8	82.2	65434	AC101467	AC101467 Mus muscu
441	14.8	82.2	2463	6	AX684714	AX684714 Sequence	C 514	14.8	82.2	68291	BX897675	BX897675 Neurospor
442	14.8	82.2	2466	6	AX523715	AX523715 Sequence	C 515	14.8	82.2	68343	AC139665	AC139665 Homo sapi
443	14.8	82.2	2526	6	AX523742	AX523742 Sequence	C 516	14.8	82.2	68531	AC055868	AC055868 Homo sapi
444	14.8	82.2	2532	6	AX523743	AX523743 Sequence	C 517	14.8	82.2	68531	AC055868	AC055868 Homo sapi
445	14.8	82.2	2630	10	BC064659	BC064659 Rattus no	C 518	14.8	82.2	68631	AL139348	AL139348 Human DNA
446	14.8	82.2	2654	4	AY297040	AY297040 Bos tauru	C 519	14.8	82.2	70269	AC100921	AC100921 Mus muscu
447	14.8	82.2	2706	4	AY297041S3	AY297041S3 Bos tauru	C 520	14.8	82.2	70276	AC101253	AC101253 Mus muscu
448	14.8	82.2	2728	5	BC068910	BC068910 Xenopus l	C 521	14.8	82.2	71169	AL139399	AL139399 Human DNA
449	14.8	82.2	2743	6	CQ597023	CQ597023 Sequence	C 522	14.8	82.2	72592	AC067876	AC067876 Homo sapi
450	14.8	82.2	2900	6	CQ597558	CQ597558 Sequence	C 523	14.8	82.2	74337	AL136082	AL136082 Human DNA
451	14.8	82.2	3258	5	BC046860	BC046860 Xenopus l	C 524	14.8	82.2	75604	BX293551	BX293551 Mouse DNA
452	14.8	82.2	3419	10	BC013766	BC013766 Mus muscu	C 525	14.8	82.2	78086	AC100634	AC100634 Mus muscu
453	14.8	82.2	3445	8	SCYGR157M	SCYGR157M S.cerevisia	C 526	14.8	82.2	78635	AL662820	AL662820 Human DNA
454	14.8	82.2	3882	8	YSCPEMA	YSCPEMA M16987 Yeast (S.ce	C 527	14.8	82.2	78812	AC107211	AC107211 Homo sapi
455	14.8	82.2	3916	8	EMCALCR	EMCALCR M24071 Emericella	C 528	14.8	82.2	78812	AC125283	AC125283 Homo sapi
456	14.8	82.2	4236	3	AB107322	AB107322 Drosophil	C 529	14.8	82.2	79661	AL359758	AL359758 Human DNA
457	14.8	82.2	4236	3	AB107342	AB107342 Drosophil	C 530	14.8	82.2	81000	AB038161	AB038161 Homo sapi

531	14.8	82.2	82453	9	AC004558	AC004558 Homo sapi
532	14.8	82.2	82674	9	AF186999	AF186999 Homo sapi
533	14.8	82.2	82676	9	AC103956	AC103956 Homo sapi
534	14.8	82.2	83848	10	AC097143	AC097143 Rattus no
535	14.8	82.2	84252	9	AC009207	AC009207 Drosophill
536	14.8	82.2	84912	9	AF024533	AF024533 Homo sapi
537	14.8	82.2	86441	2	AL330762	AL330762 Homo sapi
538	14.8	82.2	87370	2	AL336412	AL336412 Homo sapi
539	14.8	82.2	88516	2	AC129562	AC129562 Mus muscu
540	14.8	82.2	89678	9	AC006153	AC006153 Homo sapi
541	14.8	82.2	90252	9	AC069008	AC069008 Homo sapi
542	14.8	82.2	90785	2	AC149888	AC149888 Xenopus t
543	14.8	82.2	91792	9	AC092355	AC092355 Homo sapi
544	14.8	82.2	94036	8	AP004081	AP004081 Oryza sat
545	14.8	82.2	94170	9	AC068777	AC068777 Homo sapi
546	14.8	82.2	95614	2	AC012890	AC012890 Drosophill
547	14.8	82.2	97544	8	AP006675	AP006675 Lotus cor
548	14.8	82.2	97761	2	AC133737	AC133737 Rattus no
549	14.8	82.2	98393	2	AC150179	AC150179 Gallus ga
550	14.8	82.2	10000	9	AP000519	AP000519 Homo sapi
551	14.8	82.2	100183	9	EX088647	EX088647 Human DNA
552	14.8	82.2	100314	8	MTFACG	X55026 Fodopora a
553	14.8	82.2	100697	5	AL672072	AL672072 Zebrafish
554	14.8	82.2	101243	9	AC117458	AC117458 Homo sapi
555	14.8	82.2	101470	9	CR388205	CR388205 Human DNA
556	14.8	82.2	103695	9	AC010437	AC010437 Homo sapi
557	14.8	82.2	104485	10	AB114903	AB114903 Mus muscu
558	14.8	82.2	104577	5	AL713869	AL713869 Zebrafish
559	14.8	82.2	105837	5	EX470136	EX470136 Zebrafish
560	14.8	82.2	106123	9	AC109821	AC109821 Homo sapi
561	14.8	82.2	107095	10	AL671331	AL671331 Mouse DNA
562	14.8	82.2	107260	9	AL139352	AL139352 Human DNA
563	14.8	82.2	108245	9	AC005166	AC005166 Homo sapi
564	14.8	82.2	109528	1	AF040570	AF040570 Amycolato
565	14.8	82.2	110000	2	AC087331_2	Continuation (3 of
566	14.8	82.2	110000	2	AC094244_1	Continuation (2 of
567	14.8	82.2	110000	2	AC098192_1	Continuation (2 of
568	14.8	82.2	110000	2	AC098193_5	Continuation (6 of
569	14.8	82.2	110000	2	AC102028_0	AC102028 Mus muscu
570	14.8	82.2	110000	2	AC127191_1	Continuation (2 of
571	14.8	82.2	110000	2	AC127735_2	Continuation (3 of
572	14.8	82.2	110000	2	AC127735_3	Continuation (4 of
573	14.8	82.2	110000	8	CR380956_05	Continuation (17 of
574	14.8	82.2	110000	8	CR382126_16	Continuation (24 o
575	14.8	82.2	110000	8	CR382128_23	Continuation (24 o
576	14.8	82.2	110445	2	AC018587	AC018587 Homo sapi
577	14.8	82.2	110794	9	AL662827	AL662827 Human DNA
578	14.8	82.2	112626	9	EX927229	EX927229 Human DNA
579	14.8	82.2	114020	10	AC127596	AC127596 Mus muscu
580	14.8	82.2	114103	5	AL672171	AL672171 Zebrafish
581	14.8	82.2	114269	2	AP002341	AP002341 Homo sapi
582	14.8	82.2	114575	9	EX248088	EX248088 Human DNA
583	14.8	82.2	114842	9	AC002996	AC002996 Homo sapi
584	14.8	82.2	115345	9	AC008147	AC008147 Homo sapi
585	14.8	82.2	115863	9	H2268D13	AC023513 Human DNA
586	14.8	82.2	116803	9	AC131904	AC131904 Homo sapi
587	14.8	82.2	116929	2	AL356001	AL356001 Homo sapi
588	14.8	82.2	118319	2	AC141829	AC141829 Apis mell
589	14.8	82.2	119211	6	AR408761	AR408761 Sequence
590	14.8	82.2	119211	6	AR067465	AR067465 Sequence
591	14.8	82.2	120065	9	AC109495	AC109495 Homo sapi
592	14.8	82.2	120391	2	AC017146	AC017146 Drosophill
593	14.8	82.2	121659	8	AC137001	AC137001 Oryza sat
594	14.8	82.2	121896	9	AL138713	AL138713 Human DNA
595	14.8	82.2	122114	2	AC007573	AC007573 Drosophill
596	14.8	82.2	122240	9	AF238380	AF238380 Homo sapi
597	14.8	82.2	122928	8	AC002387	AC002387 Arabidops
598	14.8	82.2	123880	2	AC117928	AC117928 Gallus ga
599	14.8	82.2	123943	10	AL592547	AL592547 Mouse DNA
600	14.8	82.2	124095	9	AC002477	AC002477 Human PAC
601	14.8	82.2	125000	8	CNS08CB0	AL844877 Oryza sat
602	14.8	82.2	127342	9	AC139718	AC139718 Homo sapi
603	14.8	82.2	127553	2	AC022835	AC022835 Homo sapi

604	14.8	82.2	127953	2	AC022835	AC022835 Homo sapi
605	14.8	82.2	128991	10	AC117775	AC117775 Mus muscu
606	14.8	82.2	128611	9	AL645935	AL645935 Human DNA
607	14.8	82.2	129984	2	AC148211	AC148211 Dasypus n
608	14.8	82.2	130280	9	AC147087	AC147087 Pan trogl
609	14.8	82.2	130609	2	AC023217	AC023217 Homo sapi
610	14.8	82.2	132585	9	AC131947	AC131947 Homo sapi
611	14.8	82.2	133144	2	AC015424	AC015424 Drosophill
612	14.8	82.2	133207	9	AL157413	AL157413 Human DNA
613	14.8	82.2	133534	10	AL929233	AL929233 Mouse DNA
614	14.8	82.2	134084	9	AC004966	AC004966 Homo sapi
615	14.8	82.2	134907	8	AP005303	AP005303 Oryza sat
616	14.8	82.2	135070	2	AP003741	AP003741 Oryza sat
617	14.8	82.2	135278	2	AC109145	AC109145 Mus muscu
618	14.8	82.2	135511	8	AP005097	AP005097 Oryza sat
619	14.8	82.2	136410	2	AC146816	AC146816 Oryza sat
620	14.8	82.2	136725	9	AC074000	AC074000 Homo sapi
621	14.8	82.2	136725	9	AC026369	AC026369 Homo sapi
622	14.8	82.2	137651	8	AC130600	AC130600 Oryza sat
623	14.8	82.2	137676	2	AC147763	AC147763 Dasypus n
624	14.8	82.2	138176	5	AL145791	AL145791 Xenopus t
625	14.8	82.2	138341	5	AL935053	AL935053 Zebrafish
626	14.8	82.2	138419	10	AC111060	AC111060 Mus muscu
627	14.8	82.2	138621	9	AP002028	AP002028 Homo sapi
628	14.8	82.2	139035	9	AL356102	AL356102 Human DNA
629	14.8	82.2	139055	2	CR388100	CR388100 Dantio rer
630	14.8	82.2	139471	2	AC139982	AC139982 Rattus no
631	14.8	82.2	139793	9	AC125629	AC125629 Homo sapi
632	14.8	82.2	140168	2	AC021783	AC021783 Homo sapi
633	14.8	82.2	140729	8	AP006548	AP006548 Oryza sat
634	14.8	82.2	140952	2	AC027182	AC027182 Homo sapi
635	14.8	82.2	141120	9	AC002528	AC002528 Human BAC
636	14.8	82.2	141233	2	AC149947	AC149947 Strongylio
637	14.8	82.2	141233	2	AC149947	AC149947 Strongylio
638	14.8	82.2	141924	2	AL138830	AL138830 Human DNA
639	14.8	82.2	142133	9	AC135014	AC135014 Felle cat
640	14.8	82.2	142475	9	AC073525	AC073525 Homo sapi
641	14.8	82.2	142841	9	AC132368	AC132368 Homo sapi
642	14.8	82.2	143084	9	AC034200	AC034200 Homo sapi
643	14.8	82.2	143269	2	AC115004	AC115004 Mus muscu
644	14.8	82.2	143572	10	AL844168	AL844168 Mouse DNA
645	14.8	82.2	143655	2	AC010808	AC010808 Homo sapi
646	14.8	82.2	144076	8	AP005764	AP005764 Oryza sat
647	14.8	82.2	144087	9	AP001621	AP001621 Homo sapi
648	14.8	82.2	144552	3	AC007725	AC007725 Drosophill
649	14.8	82.2	144353	9	AL670405	AL670405 Human DNA
650	14.8	82.2	144940	2	AC102415	AC102415 Mus muscu
651	14.8	82.2	145068	9	HSDJ977B1	AL050318 Human DNA
652	14.8	82.2	145177	8	AP004708	AP004708 Oryza sat
653	14.8	82.2	145263	10	BX005039	BX005039 Mouse DNA
654	14.8	82.2	145293	9	HS64411	AL035665 Human DNA
655	14.8	82.2	145729	9	AC117489	AC117489 Homo sapi
656	14.8	82.2	146052	2	CR394049	CR394049 Dantio rer
657	14.8	82.2	146180	9	AC007193	AC007193 Homo sapi
658	14.8	82.2	147164	10	AC138597	AC138597 Mus muscu
659	14.8	82.2	147460	5	BX322595	BX322595 Zebrafish
660	14.8	82.2	147639	9	AC148704	AC148704 Macaca mu
661	14.8	82.2	148337	2	AC021599	AC021599 Homo sapi
662	14.8	82.2	148348	8	AC108498	AC108498 Oryza sat
663	14.8	82.2	148598	9	HSEAS1C14	AL121878 Human DNA
664	14.8	82.2	148740	10	AL928931	AL928931 Mouse DNA
665	14.8	82.2	148783	9	AC068570	AC068570 Homo sapi
666	14.8	82.2	149490	2	AL589985	AL589985 Homo sapi
667	14.8	82.2	149850	9	AP001622	AP001622 Homo sapi
668	14.8	82.2	149850	9	AP001622	AP001622 Homo sapi
669	14.8	82.2	150023	2	AP001811	AP001811 Homo sapi
670	14.8	82.2	150102	2	EX957301	EX957301 Dantio rer
671	14.8	82.2	150354	9	AC091920	AC091920 Homo sapi
672	14.8	82.2	150399	2	AC009369	AC009369 Drosophill
673	14.8	82.2	151080	2	AC093219	AC093219 Homo sapi
674	14.8	82.2	151084	2	AC113326	AC113326 Homo sapi
675	14.8	82.2	151108	2	AC024450	AC024450 Homo sapi
676	14.8	82.2	151133	9	AC013355	AC013355 Homo sapi

C 677	14.8	82.2	151214	9	AC099048	Homo sapi	AL845502	10	AL845502	Mouse DNA
C 678	14.8	82.2	151750	9	AC003666	Homo sapi	AL148919	5	AL148919	Gallus ga
C 679	14.8	82.2	151753	2	AC119614	Rattus no	AL354937	2	AL354937	Human DNA
C 680	14.8	82.2	151861	10	AC127546	Mus muscu	AL127546	2	AC073136	Homo sapi
C 681	14.8	82.2	152057	9	AL139344	Human DNA	AL139344	9	AC099057	Homo sapi
C 682	14.8	82.2	152342	2	AC135872	Rattus no	AL135872	2	CR376729	Danio rer
C 683	14.8	82.2	152351	2	AC073914	Homo sapi	AC135872	2	CR376729	Danio rer
C 684	14.8	82.2	152797	2	AC012134	Homo sapi	AC104155	2	AC104155	Pan trogl
C 685	14.8	82.2	153071	2	AC104155	Pan trogl	AC104155	2	AC104155	Pan trogl
C 686	14.8	82.2	153311	2	AC016836	Homo sapi	AC104155	2	AC104155	Pan trogl
C 687	14.8	82.2	153455	2	AC145260	Felis cat	AC145260	2	AC145260	Felis cat
C 688	14.8	82.2	153475	2	AP005710	Oryza sat	AP005710	2	AP005710	Oryza sat
C 689	14.8	82.2	153728	10	AP003449	Mus muscu	AP003449	10	AP003449	Mus muscu
C 690	14.8	82.2	154091	2	AP003819	Oryza sat	AP003819	2	AP003819	Oryza sat
C 691	14.8	82.2	154413	2	AC007862	Trypanoso	AC007862	2	AC007862	Trypanoso
C 692	14.8	82.2	154440	2	AC130438	Homo sapi	AC130438	2	AC130438	Homo sapi
C 693	14.8	82.2	154441	8	AP005383	Oryza sat	AP005383	8	AP005383	Oryza sat
C 694	14.8	82.2	154462	2	AC031636	Homo sapi	AC031636	2	AC031636	Homo sapi
C 695	14.8	82.2	154788	2	AC031384	Homo sapi	AC031384	2	AC031384	Homo sapi
C 696	14.8	82.2	154922	9	AC090842	Homo sapi	AC090842	9	AC090842	Homo sapi
C 697	14.8	82.2	154980	5	AC147353	Xenopus t	AC147353	5	AC147353	Xenopus t
C 698	14.8	82.2	154982	9	AC146436	Pan trogl	AC146436	9	AC146436	Pan trogl
C 699	14.8	82.2	155000	2	AC023689	Drosophil	AC023689	2	AC023689	Drosophil
C 700	14.8	82.2	155239	2	AC013818	Homo sapi	AC013818	2	AC013818	Homo sapi
C 701	14.8	82.2	155751	10	AC132347	Mus muscu	AC132347	10	AC132347	Mus muscu
C 702	14.8	82.2	156332	10	AC115581	Mus muscu	AC115581	10	AC115581	Mus muscu
C 703	14.8	82.2	156557	2	CR405705	Danio rer	CR405705	2	CR405705	Danio rer
C 704	14.8	82.2	156602	9	AC012487	Homo sapi	AC012487	9	AC012487	Homo sapi
C 705	14.8	82.2	156801	5	AL929467	Zebrafish	AL929467	5	AL929467	Zebrafish
C 706	14.8	82.2	157023	2	AC013625	Homo sapi	AC013625	2	AC013625	Homo sapi
C 707	14.8	82.2	157029	9	AL135796	Human DNA	AL135796	9	AL135796	Human DNA
C 708	14.8	82.2	157063	10	AL928950	Mouse DNA	AL928950	10	AL928950	Mouse DNA
C 709	14.8	82.2	157068	2	AC018405	Homo sapi	AC018405	2	AC018405	Homo sapi
C 710	14.8	82.2	157083	2	AC14692	Apis mell	AC14692	2	AC14692	Apis mell
C 711	14.8	82.2	157101	2	AC145541	Oryctolag	AC145541	2	AC145541	Oryctolag
C 712	14.8	82.2	157189	3	AC008307	Drosophil	AC008307	3	AC008307	Drosophil
C 713	14.8	82.2	157739	9	AP001623	Homo sapi	AP001623	9	AP001623	Homo sapi
C 714	14.8	82.2	157750	2	AC006097	Homo sapi	AC006097	2	AC006097	Homo sapi
C 715	14.8	82.2	157910	2	AC124981	Homo sapi	AC124981	2	AC124981	Homo sapi
C 716	14.8	82.2	158006	2	AC026345	Homo sapi	AC026345	2	AC026345	Homo sapi
C 717	14.8	82.2	158014	2	AC092413	Felis cat	AC092413	2	AC092413	Felis cat
C 718	14.8	82.2	158027	10	AC125093	Mus muscu	AC125093	10	AC125093	Mus muscu
C 719	14.8	82.2	158033	9	AC018926	Homo sapi	AC018926	9	AC018926	Homo sapi
C 720	14.8	82.2	158108	10	AL807780	Mouse DNA	AL807780	10	AL807780	Mouse DNA
C 721	14.8	82.2	158479	8	AP003856	Oryza sat	AP003856	8	AP003856	Oryza sat
C 722	14.8	82.2	158526	10	AC112330	Rattus no	AC112330	10	AC112330	Rattus no
C 723	14.8	82.2	158637	2	AC141226	Homo sapi	AC141226	2	AC141226	Homo sapi
C 724	14.8	82.2	158698	2	AC018625	Homo sapi	AC018625	2	AC018625	Homo sapi
C 725	14.8	82.2	158871	9	AL354833	Human DNA	AL354833	9	AL354833	Human DNA
C 726	14.8	82.2	158978	2	AC136597	Homo sapi	AC136597	2	AC136597	Homo sapi
C 727	14.8	82.2	159178	9	AL669914	Human DNA	AL669914	9	AL669914	Human DNA
C 728	14.8	82.2	159305	9	AC097633	Homo sapi	AC097633	9	AC097633	Homo sapi
C 729	14.8	82.2	159349	9	AC097633	Homo sapi	AC097633	9	AC097633	Homo sapi
C 730	14.8	82.2	159427	9	AL845454	Human DNA	AL845454	9	AL845454	Human DNA
C 731	14.8	82.2	159520	9	AC013009	Homo sapi	AC013009	9	AC013009	Homo sapi
C 732	14.8	82.2	159791	9	AC024451	Homo sapi	AC024451	9	AC024451	Homo sapi
C 733	14.8	82.2	159804	10	AL929215	Mouse DNA	AL929215	10	AL929215	Mouse DNA
C 734	14.8	82.2	160010	2	AC019333	Homo sapi	AC019333	2	AC019333	Homo sapi
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C 736	14.8	82.2	160207	10	AC121859	Mus muscu	AC121859	10	AC121859	Mus muscu
C 737	14.8	82.2	160238	10	AC133502	Mus muscu	AC133502	10	AC133502	Mus muscu
C 738	14.8	82.2	160386	2	AC102379	Mus muscu	AC102379	2	AC102379	Mus muscu
C 739	14.8	82.2	160505	9	AC122720	Homo sapi	AC122720	9	AC122720	Homo sapi
C 740	14.8	82.2	160541	2	AL359271	Homo sapi	AL359271	2	AL359271	Homo sapi
C 741	14.8	82.2	160764	10	RN120J22	Rattus no	RN120J22	10	RN120J22	Rattus no
C 742	14.8	82.2	161725	2	AC084000	Homo sapi	AC084000	2	AC084000	Homo sapi
C 743	14.8	82.2	161817	10	AC132119	Mus muscu	AC132119	10	AC132119	Mus muscu
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C 745	14.8	82.2	162150	9	AC093877	Homo sapi	AC093877	9	AC093877	Homo sapi
C 746	14.8	82.2	162227	9	AB023056	Homo sapi	AB023056	9	AB023056	Homo sapi
C 747	14.8	82.2	162426	2	AC011858	Homo sapi	AC011858	2	AC011858	Homo sapi
C 748	14.8	82.2	162923	3	AC008236	Drosophil	AC008236	3	AC008236	Drosophil
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823	14.8	82.2	175924	2	BX927301	BX927301	Danio rer	C 856	14.8	82.2	185960	2	BX004757	BX004757	Mus muscu
824	14.8	82.2	176184	9	AC018845	AC018845	Homo sapi	C 897	14.8	82.2	187081	10	AC124421	AC124421	Mus muscu
825	14.8	82.2	176233	3	AC023690	AC023690	Drosophi	C 898	14.8	82.2	187277	9	AC022968	AC022968	Homo sapi
826	14.8	82.2	176258	5	AL954175	AL954175	Zebrafish	C 899	14.8	82.2	187418	10	AL672278	AL672278	Mouse DNA
827	14.8	82.2	176345	2	AC132913	AC132913	Mus muscu	C 900	14.8	82.2	187911	2	AC136867	AC136867	Rattus no
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829	14.8	82.2	176752	2	BX927231	BX927231	Danio rer	C 902	14.8	82.2	188349	9	AL390197	AL390197	Human DNA
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831	14.8	82.2	176844	2	AC120333	AC120333	Rattus no	C 904	14.8	82.2	188772	10	AL773525	AL773525	Mouse DNA
832	14.8	82.2	176851	2	AC106372	AC106372	Homo sapi	C 905	14.8	82.2	189056	2	AC017052	AC017052	Homo sapi
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834	14.8	82.2	177063	2	AC103624	AC103624	Mus muscu	C 907	14.8	82.2	189424	2	AC148512	AC148512	Fapio anu
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839	14.8	82.2	178676	2	AC120499	AC120499	Papio ham	C 912	14.8	82.2	190828	2	AC164604	AC164604	Mus muscu
840	14.8	82.2	178787	2	AC113134	AC113134	Homo sapi	C 913	14.8	82.2	190828	2	AL683814	AL683814	Mouse DNA
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842	14.8	82.2	178931	10	AC092514	AC092514	Papio anu	C 915	14.8	82.2	191300	2	AC118937	AC118937	Mus muscu
843	14.8	82.2	179080	2	AC092514	AC092514	Papio anu	C 916	14.8	82.2	191655	9	AC020661	AC020661	Homo sapi
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849	14.8	82.2	179683	2	AC115823	AC115823	Mus muscu	C 922	14.8	82.2	193012	2	AC146779	AC146779	Papio anu
850	14.8	82.2	179915	10	AC124347	AC124347	Mus muscu	C 923	14.8	82.2	193016	2	AC149863	AC149863	Papio anu
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852	14.8	82.2	180016	9	AC023090	AC023090	Homo sapi	C 925	14.8	82.2	193304	2	AC118868	AC118868	Rattus no
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854	14.8	82.2	180252	10	AL844538	AL844538	Mouse DNA	C 927	14.8	82.2	193775	2	AC123129	AC123129	Rattus no
855	14.8	82.2	180290	2	AC123434	AC123434	Rattus no	C 928	14.8	82.2	193933	2	AC140928	AC140928	Mus muscu
856	14.8	82.2	180563	2	AC146160	AC146160	Pan trogl	C 929	14.8	82.2	193991	9	AC113209	AC113209	Homo sapi
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864	14.8	82.2	181557	2	AC072055	AC072055	Homo sapi	C 937	14.8	82.2	194991	2	AC102735	AC102735	Mus muscu
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867	14.8	82.2	182439	10	AL805955	AL805955	Mouse DNA	C 940	14.8	82.2	195342	10	AC128739	AC128739	Mus muscu
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870	14.8	82.2	183068	2	CR354422	CR354422	Danio rer	C 943	14.8	82.2	196204	9	AC073957	AC073957	Homo sapi
871	14.8	82.2	183167	2	AC122988	AC122988	Rattus no	C 944	14.8	82.2	196791	2	AC118298	AC118298	Mus muscu
872	14.8	82.2	183291	3	AC010003	AC010003	Drosophi	C 945	14.8	82.2	196904	10	AL513346	AL513346	Mouse DNA
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878	14.8	82.2	184194	2	AC022805	AC022805	Homo sapi	C 951	14.8	82.2	197597	2	AC102335	AC102335	Mus muscu
879	14.8	82.2	184211	2	AC146112	AC146112	Pan trogl	C 952	14.8	82.2	197597	2	AC102335	AC102335	Mus muscu
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881	14.8	82.2	184618	10	AC123053	AC123053	Mus muscu	C 954	14.8	82.2	197981	2	AC117089	AC117089	Rattus no
882	14.8	82.2	184869	10	AC122325	AC122325	Mus muscu	C 955	14.8	82.2	198068	9	AC087240	AC087240	Homo sapi
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884	14.8	82.2	185173	2	AC009056	AC009056	Homo sapi	C 957	14.8	82.2	198176	8	ATCHR1V17	ATCHR1V17	Mouse DNA
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894	14.8	82.2	186604	9	AC139887	AC139887	Homo sapi	C 967	14.8	82.2	199280	2	AC114586	AC114586	Mus muscu
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969 14.8 82.2 199808 10 AC103600  
 c 970 14.8 82.2 199820 5 BX294113  
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 972 14.8 82.2 200274 9 AC115088  
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 976 14.8 82.2 200491 9 AC007249  
 977 14.8 82.2 200548 2 AC040962  
 c 978 14.8 82.2 200567 2 AP001587  
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 981 14.8 82.2 200956 9 AC104165  
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 c 984 14.8 82.2 201436 10 AC131920  
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 c 989 14.8 82.2 202322 2 AC117316  
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 c 998 14.8 82.2 204495 10 AL591884  
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## ALIGNMENTS

RESULT 1  
 AX481362  
 LOCUS AX481362 18 bp DNA linear PAT 16-AUG-2002  
 DEFINITION Sequence 9 from Patent EP1225232.  
 ACCESSION AX481362  
 VERSION AX481362.1 GI:22316283  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 RUBIN,B.Y. and Anderson,S.L.  
 Detection of mutations in a gene encoding lkappab  
 kinase-complex-associated protein to diagnose familial dysautonomia  
 Patent: EP 1225232-A 9 24-JUL-2002;  
 RUBIN, Berish Y. (US); Anderson, Silvia L. (US)  
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 1. .18  
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## ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;  
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 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTTGGTACTTGGCTG 18  
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## RESULT 2

AX676048/c  
 LOCUS AX676048 66479 bp DNA linear PAT 27-MAR-2003

DEFINITION Sequence 1 from Patent WO02059381.  
 ACCESSION AX676048  
 VERSION AX676048.1 GI:29333739  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 Slagenhaupt,S. and Gusella,J.F.  
 Gene for identifying individuals with familial dysautonomia  
 Patent: WO 02059381-A 1 01-AUG-2002;  
 The General Hospital Corporation (US)

## FEATURES

source  
 1. .66479  
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## ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 66479;  
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## Qy

1 ATGCTTGGTACTTGGCTG 18  
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## RESULT 3

AL359692  
 LOCUS Human DNA sequence from clone RP11-3J11 on chromosome 9, complete  
 DEFINITION sequence.  
 ACCESSION AL359692  
 VERSION AL359692.9 GI:14970800  
 KEYWORDS HTG.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 Sycamore,N.  
 Direct Submission  
 Submitted (18-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
 requests: clonerequest@sanger.ac.uk

On Jul 19, 2001 this sequence version replaced gi:14715342.

During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 This sequence was finished as follows unless otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest. The following  
 abbreviations are used to associate primary accession numbers given  
 in the feature table with their source databases: Em:, EMBL; Swi:,  
 SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP  
 database can be found at  
[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence  
 was generated from part of bacterial clone contigs of human  
 chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping  
 Group. Further information can be found at  
<http://www.sanger.ac.uk/HGP/Chr9>  
 RP11-3J11 is from the library RPI1-11.1 constructed by the group of  
 Pieter de Jong. For further details see  
<http://www.chori.org/bacpac/home.htm>

## COMMENT



## VECTOR: pBAC3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-3J11. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-3J11 is at 1 in this sequence. The true left end of clone RP11-115J22 is at 76377 in this sequence. The true right end of clone RP11-339N8 is at 76382 in this sequence.

## FEATURES

## Location/Qualifiers

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 /clone\_lib="RPCI-11.1"

7. 829  
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 991. 1328  
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 2199. .2234  
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 3191. .3349  
 /note="AluSg/x repeat: matches 153. .311 of consensus"  
 4250. 4537  
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 5314. 5579  
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 5693. 5863  
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 5881. 6013  
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 6533. 6644  
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 9165. 9774  
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 9775. 9848  
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 9849. 10232  
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 10233. 10535  
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 10536. 10668  
 /note="MER84 repeat: matches 373. .508 of consensus"  
 10669. 10846  
 /note="MER21B repeat: matches 7. .185 of consensus"  
 11168. 11901  
 /note="L1PA14 repeat: matches 5403. .6149 of consensus"  
 12172. 12468  
 /note="AluSg repeat: matches 1. .297 of consensus"  
 13074. 13362  
 /note="AluSx repeat: matches 3. .294 of consensus"  
 13411. 13533  
 /note="MIR repeat: matches 117. .239 of consensus"  
 13616. 13669  
 /note="L2 repeat: matches 2445. .2498 of consensus"  
 13733. 13841  
 /note="MER33 repeat: matches 89. .188 of consensus"  
 13936. 14113  
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 14769. 15142  
 /note="MSTA repeat: matches 1. .423 of consensus"  
 15274. 15333  
 /note="MER3A repeat: matches 14. .74 of consensus"  
 15480. 15600  
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 15640. 15689  
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 15881. 16180  
 /note="AluY repeat: matches 1. .302 of consensus"  
 17189. 17296

repeat\_region  
 /note="MIR repeat: matches 100. .206 of consensus"  
 17614. 17738  
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 17769. 18234  
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 18235. 18529  
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 40477. 40798  
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/note="L1ME2 repeat: matches 6041..6161 of consensus"
41739..41805
/note="RIGER2 repeat: matches 2653..2718 of consensus"
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/note="Aluub repeat: matches 1..300 of consensus"
42094..43429
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43429..44232
/note="RIGER2 repeat: matches 297..1113 of consensus"
44353..44664

Query Match      100.0%; Score 18; DB 9; Length 78376;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGCTTGCTACTGGCTG 18
Db      72029 ATGCTTGCTACTGGCTG 72046

RESULT 4
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LOCUS      AC119879      44415 bp      DNA      linear      HTG 02-MAY-2002
DEFINITION Mus musculus clone RP24-40906, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC119879
VERSION AC119879.1 GI:20389537
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
Birken,B., Linton,L., Nusbaum,C. and Lander,E.
1 (bases 1 to 44415)
Mus musculus, clone RP24-40906
Unpublished
2 (bases 1 to 44415)
Birken,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Chopel,Y., Colangelo,M., Collins,S., Collamore,A.,
Cook,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazates,R.,
Landers,T., Lehoczyk,J., Levine,R., Lindblad-Toh,K., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,C.,
Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (02-MAY-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
----- Project name: L24817

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Center clone name: 409\_O\_6

NOTE: This record contains 55 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.

1 708: contig of 708 bp in length  
709 808: gap of 100 bp  
809 1512: contig of 704 bp in length  
1513 1612: gap of 100 bp  
1613 2328: contig of 716 bp in length  
2329 2429: gap of 100 bp  
2429 3140: contig of 712 bp in length  
3141 3240: gap of 100 bp  
3241 3343: contig of 703 bp in length  
3343 3944: gap of 100 bp  
3944 4044: contig of 712 bp in length  
4044 4756: gap of 100 bp  
4756 5569: contig of 714 bp in length  
5570 5669: gap of 100 bp  
5670 6384: contig of 715 bp in length  
6385 6484: gap of 100 bp  
6485 7193: contig of 709 bp in length  
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7294 7878: contig of 685 bp in length  
7879 8786: gap of 100 bp  
8787 8886: contig of 708 bp in length  
8887 8986: gap of 100 bp  
8987 9585: contig of 699 bp in length  
9586 10371: contig of 686 bp in length  
10372 11071: gap of 100 bp  
11072 11203: contig of 732 bp in length  
11204 12007: contig of 704 bp in length  
12008 12108: contig of 731 bp in length  
12109 12338: gap of 100 bp  
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14585 15269: contig of 685 bp in length  
15270 15369: gap of 100 bp  
15370 16087: contig of 718 bp in length  
16088 16187: gap of 100 bp  
16188 16898: contig of 711 bp in length  
16899 16998: gap of 100 bp  
16999 17704: contig of 706 bp in length  
17705 18517: contig of 713 bp in length  
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19345 19444: gap of 100 bp  
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21051 21745: contig of 695 bp in length  
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26614 26713: gap of 100 bp  
26714 27420: contig of 707 bp in length  
27421 27520: gap of 100 bp  
27521 28215: contig of 695 bp in length  
28216 28315: gap of 100 bp  
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29042 29141: gap of 100 bp  
29142 29859: contig of 718 bp in length  
29860 29959: gap of 100 bp  
29960 30666: contig of 707 bp in length  
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31478 31577: gap of 100 bp  
31578 32286: contig of 708 bp in length  
32287 32386: gap of 100 bp  
32387 33087: contig of 702 bp in length  
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33188 33914: contig of 727 bp in length  
33915 34014: gap of 100 bp  
34015 34735: contig of 721 bp in length  
34736 34835: gap of 100 bp  
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35560 36353: gap of 100 bp  
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36455 37263: contig of 709 bp in length  
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38058 38772: contig of 715 bp in length  
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Qy 2 TGCTGGTACTGGCTG 18  
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Db 19525 TGCTGGTACTGGCTG 19509

RESULT 5  
AC115935/c  
LOCUS  
DEFINITION Mus musculus chromosome 3 clone RP24-545D23 map 3, WORKING DRAFT  
SEQUENCE, 4 ordered pieces.  
AC115935

VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS

AC115935.5 GI:44866885  
HTG; HTGS\_PHASE2; HTGS\_DRAFT; HTGS\_FULLTOP.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Birren,B., Nusbaum,C. and Lander,E.  
1 (bases 1 to 146632)  
Mus musculus chromosome 3, clone RP24-545D23  
Unpublished  
2 (bases 1 to 146632)  
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,  
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L.,  
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,  
Chazaro,B., Choepel,Y., Collangelo,M., Collins,S., Collymore,A.,  
Cook,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S.,  
Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,  
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,  
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,  
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,  
Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G.,  
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Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,  
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 146632)  
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,  
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Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,  
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,  
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O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,  
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Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,  
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
Direct Submission

TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Submitted (09-MAR-2004) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 2, 2004 this sequence version replaced gi:28927771.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L24917  
Center clone name: 545.D.23  
----- Summary Statistics

TITLE  
JOURNAL  
COMMENT

Submitted (09-MAR-2004) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 2, 2004 this sequence version replaced gi:28927771.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L24917  
Center clone name: 545.D.23  
----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 144826 bases at least Q40  
 Consensus quality: 145150 bases at least Q30  
 Consensus quality: 145423 bases at least Q20  
 Insert size: 145000; agarose-fp  
 Inset size: 145642; sum-of-contigs  
 Quality coverage: 11.4 in Q20 bases; agarose-fp  
 Quality coverage: 11.4 in Q20 bases; sum-of-contigs

\*\*\*\*\*  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 4 contigs. Gaps between the contigs  
 \* are represented as runs of N. The order of the pieces  
 \* is believed to be correct as given, however the sizes  
 \* of the gaps between them are based on estimates that have  
 \* provided by the submitter.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.  
 \* 1 48025: contig of 48025 bp in length  
 \* 48026 48125: gap of 100 bp  
 \* 48126 88306: contig of 40181 bp in length  
 \* 88307 88406: gap of 100 bp  
 \* 88407 98916: contig of 10510 bp in length  
 \* 98917 98016: gap of 100 bp  
 \* 99017 146632: contig of 47616 bp in length.

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 /clone\_lib="RPCI-24 Male Mouse BAC"  
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 clone end:SP6  
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misc\_feature

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 88407..98916  
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 clone end:T7  
 vector\_side:right"

## ORIGIN

Query Match 94.4%; Score 17; DB 2; Length 146632;  
 Best Local Similarity 100.0%; Pred.No.1.2e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TCGTTGGTACTGGCTG 18

DB 8171 TCGTTGGTACTGGCTG 8155

## RESULT 6

AC116409/C

LOCUS AC116409 164176 bp DNA linear HTG 08-AUG-2004  
 DEFINITION Mus musculus chromosome 3 clone RP24-337P23 map 3, \*\*\* SEQUENCING  
 IN PROGRESS \*\*\*, 6 ordered pieces.

ACCESSION AC116409

VERSION AC116409.6 GI:45384689

KEYWORDS HTG; HTGS PHASE2; HTGS\_FUZZTOP; HTGS\_ACTIVEFIN.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 164176)

AUTHORS Birren,B., Nusbaum,C. and Lander,E.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Mus musculus chromosome 3, clone RP24-337P23  
 Unpublished  
 2 (bases 1 to 164176)  
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,  
 Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L.,  
 Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,  
 Chararo,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,  
 Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,  
 Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,  
 Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,  
 Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,  
 Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,  
 Landers,T., Lehoczyk,J., Levine,R., Lindblad-Toh,K., Liu,G.,  
 Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,  
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 Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,  
 Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,  
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 Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,  
 Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R.,  
 Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,  
 Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,  
 Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,  
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 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

Direct Submission  
 Submitted (27-MAR-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 164176)  
 Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,  
 Anderson,S., Barna,N., Bastien,V., Bloom,T., Boukhgalter,B.,  
 Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,  
 Choepel,Y., Collymore,A., Cooke,P., Corum,B.,  
 DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L.,  
 Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D.,  
 Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hagos,B.,  
 Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I.,  
 Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T.,  
 Levine,R., Lindblad-Toh,K., Liu,G., Liu,A., Mabbitt,R.,  
 Maclean,C., Macdonald,P., Major,J., Manning,J., Matthews,C.,  
 McCarthy,M., Meldrum,J., Meneus,I., Mihova,T., Mlenga,V.,  
 Murphy,T., Naylor,J., Nguyen,C., Nguyen,T., Nicol,R., Norbu,C.,  
 O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,  
 Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C.,  
 Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupack,R.,  
 Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,  
 Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J.,  
 Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R.,  
 Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L.,  
 Zimmer,A. and Zody,M.

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

Direct Submission  
 Submitted (08-AUG-2004) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Mar 12, 2004 this sequence version replaced gi:44886846.  
 All repeats were identified using RepeatMasker.  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

## COMMENT

\*\*\*\*\*  
 Center: Whitehead Institute/MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@broad.mit.edu  
 \*\*\*\*\* Project Information  
 Center project name: L24745  
 Center clone name: 337\_P\_23

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 6 contigs. Gaps between the contigs  
 \* are represented as runs of N. The order of the pieces  
 \* is believed to be correct as given, however the sizes  
 \* of the gaps between them are based on estimates that have  
 \* provided by the submitter.  
 \* This sequence will be replaced

\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1 22474: contig of 22474 bp in length  
\* 22475 22574: gap of unknown length  
\* 22575 58585: contig of 36011 bp in length  
\* 58586 58685: gap of unknown length  
\* 58686 70811: contig of 12126 bp in length  
\* 70812 70911: gap of unknown length  
\* 70912 116853: contig of 45942 bp in length  
\* 116854 149470: contig of 32517 bp in length  
\* 149471 149570: gap of unknown length  
\* 149571 164176: contig of 14606 bp in length.

FEATURES

source

1. .164176  
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/db\_xref="taxon:10090"  
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ORIGIN

Query Match 94.4%; Score 17; DB 2; Length 164176;  
Best local similarity 100.0%; Pred. No. 1.le-02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGCTGGTACTTGCGTG 18

Db 137259 TGCTGGTACTTGCGTG 137243

RESULT 7

AP005086

LOCUS

DEFINITION

AP005086 BAC00032

VERSION

AP005086.1 GI:28808836

SOURCE

Vibrio parahaemolyticus

ORGANISM

Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

Vibrionaceae; Vibrio.

REFERENCE

1

Nasu,H., Iida,T., Sugahara,T., Yamaichi,Y., Park,K.S., Yokoyama,K.,

Makino,K., Shinagawa,H. and Honda,T.

A filamentous phage associated with recent pandemic Vibrio

parahaemolyticus O3:K6 strains

J. Clin. Microbiol. 38 (6), 2156-2161 (2000)

20295086

10834969

REFERENCE

2

Makino,K., Oshima,K., Kurokawa,K., Yokoyama,K., Uda,T.,

Tagomori,K., Iijima,Y., Najima,M., Nakano,M., Yamashita,A.,

Kubota,Y., Kimura,S., Yasunaga,T., Honda,T., Shinagawa,H.,

Hattori,M. and Iida,T.

Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism

distinct from that of V cholerae

Lancet 361 (9359), 743-749 (2003)

22508454

12620739

REFERENCE

3

(bases 1 to 296100)

Hattori,M., Yamashita,A., Oshima,K. and Shiba,T.

Direct Submission

Submitted (03-APR-2002) Masahira Hattori, Kitasato Institute for

Life Sciences, Kitasato University; Kitasato 1-15-1, Sagamihara,

Kanagawa 228-8555, Japan

(E-mail:hattori@genome.ls.kitasato-u.ac.jp,

URL:http://genome.ls.kitasato-u.ac.jp/, Tel:81-42-778-8194,

Fax:81-42-778-8193)

This work was done in collaboration with Koza Makino, Ken Kurokawa,

Katsushi Yokoyama, Takayuki Uda, Kenichi Tagomori, Masatomo Najima,

Masayuki Nakano, Yoshino Kubota, Shigenobu Kimura, Teruo Yasunaga,  
Takeshi Honda, Hideo Shinagawa, Tetsuya Iida (Osaka University),  
Yoshio Iijima (Kobe Institute of Health), and supported by the  
Research for the Future Program of the Japan Society for the  
Promotion of Science. This clone was isolated from a patient  
presenting with acute gastroenteritis.

FEATURES

source

Location/Qualifiers

1. .296100

/organism="Vibrio parahaemolyticus"

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/strain="O3:K6"

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/evidence=not\_experimental

/transl\_table=11

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/db\_xref="GI:28808837"

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LRUREIFQDELLFRKNGRMELTPKASIRAKLNNIHDIDELTDMSPDSTDIKI

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KNLIVQRKVGKDMVMVKRKHPIINNESISLETIASYELAIHLQKHWNERQDKLURL

LSHGIDFKVKLTKTHINVINAVETDILLPFCSTIYIAEQGKEFSYITSDDEVFLPQ

EKEFGTYDKAYKNDPMIVLHSTISKLMNDFLDVYNNKFKDSRYEKSR"

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complement (1056. .1146)

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/product="tRNA-Ser"

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1476. .2156

/gene="VPA0603"

1476. .2156

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identity 72 in 226 aa"

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/evidence=not\_experimental

/transl\_table=11

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/db\_xref="GI:28808838"

/translation="MKVTNLFKDKVDIAISAHQSEFMNWSPTLSDYSDFLGKAQNSF

LFSNVRDHNQPAVNEEAPQAPVLOEPAQKLYDELSGKIGEVHTGDWVHVGQRI

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VSVIQLHF"

complement (2210. .3037)

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complement (2210. .3037)

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identity 61 in 272 aa"

/codon\_start=1

/evidence=not\_experimental

/transl\_table=11

/product="ABC transporter, periplasmic substrate-binding

protein"

/protein\_id="BAC61947.1"

/db\_xref="GI:28808839"

/translation="MLRTVATILLAMAYSLPSMAKEYNIQSSTSVARVMVDVLAEEYN

KNTPDNYIAVQIGSSAGITWNGKVGKMGSSRYLSTESKEDLNVPFIAYDGLAVV

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KIINDRLVSDISPNLVNYSNMVKTIVYHNTRAFISVGSVDLSVAIKIOPNFKPT

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complement (3652. .4455)
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KXTSGDFUTIAIDPTAITIPEDENMDKVARERGTYIPLGRNIPMLPRDLADNLS
LIEGEHPAICCTVTSKQVIGDDIKFFAANKSHARLAYDHVSNLENGSDAWQP
SEIATVRLDYFSLARAEKNAVVPEDREDFELSENNDVIAIHADMRRSAR
LVESMTANIRACITRERFETGVFNTHAGLKEPIEEVQVLPNPEGLTFTABIA
TLGEFAALRWLAQVTSYIDNRIRKFOAYSEVGNOPLPHYAMGLDIYATVSPIRKY
GDMNHMLKAVILDKPEVQKDDOYGEELALHKKHKAERNVSDMLVARTLADEPS
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MLNKGFDVDTALMEAPSAQVLFATMPMLKNIVRFLFEDPVVDVAGKNHTVD
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KLAQCHTFVOLPKAMTSEASAKLSKLIROODYGAIVCDPDDFRESGGRDGRD
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTTGCT 17
Db 56921 ATGCTTGCTACTTGCT 56937

RESULT 8
HS606D23T 476 bp DNA linear STS 07-SEP-1998
LOCUS H.sapiens STS from genomic clone 606D23, sequence tagged site.
DEFINITION ACCESSION AL031478
VERSION AL031478.1 GI:3581626
KEYWORDS STS; single read.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 476)
AUTHORS Deloukas,P., O'Neill,L., Holden,J., Mistry,D., Huckle,E., Taylor,R.
and Hunt,S.
Direct Submission
Submitted (01-SEP-1998) E-mail contact: humquersanger.ac.uk
Marker STS606D23T7 (Primer A : GAATGCTTGCTACTTGCTGG; Primer B :
CACAGCTCATTCATCATGAGC; amplicon size : 128 bp) is from sequence
generated from the T7 end of PAC 606D23. 606D23 is part of the
bacterial clone contigs constructed by the Chromosome 20 Mapping
Group. (http://www.sanger.ac.uk/HGP/Chr20/) 606D23 is from the
Library R2C14 constructed at the Roswell Park Cancer Institute by
the group of Peter de Jong.
For further details see http://bacpac.med.buffalo.edu/.
FEATURES
source
1..476
Location/Qualifiers
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ORIGIN
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Best Local Similarity 94.4%; Pred. No. 4.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTTGCT 18
Db 64 ATGCTTGCTACTTGCT 81

RESULT 9
AR320510 1122 bp DNA linear PAT 17-AUG-2003
LOCUS AR320510
DEFINITION Sequence 3060 from patent US 6562958.
ACCESSION AR320510
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VERSION	AR320510.1	GI:33701613	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1122)		
AUTHORS	Breton, G. and Bush, D.		
TITLE	Nucleic acid and amino acid sequences relating to Acinetobacter baumannii for diagnostics and therapeutics		
JOURNAL	Patent: US 6562958-A 3060 13-MAY-2003;		
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Db	764	ATGCTTGCTACTTGCTG 781	
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DEFINITION	(habe) gene, complete cds.		
ACCESSION	AF355751		
VERSION	AF355751.1	GI:14133594	
KEYWORDS	Pseudomonas fluorescens		
SOURCE	Pseudomonas fluorescens		
ORGANISM	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.		
REFERENCE	1 (bases 1 to 1923)		
AUTHORS	Kamerbeek, N.M., Moonen, M.J., Van Der Ven, J.G., Van Berkel, W.J., Fraaije, M.W. and Janssen, D.B.		
TITLE	4-Hydroxyacetophenone monooxygenase from Pseudomonas fluorescens ACB. A novel flavoprotein catalyzing Baeyer-Villiger oxidation of aromatic compounds		
JOURNAL	Eur. J. Biochem. 268 (9), 2547-2557 (2001)		
MEDLINE	21233008		
PUBMED	11322873		
REFERENCE	2 (bases 1 to 1923)		
AUTHORS	Kamerbeek, N.M., Moonen, M.J., van der Ven, J.G., van Berkel, W.J., Fraaije, M.W. and Janssen, D.B.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-MAR-2001) Biochemistry, University of Groningen, Groningen Biomolecular Sciences and Biotechnology Institute, Nijenborgh 4, Groningen 9747 AG, Netherlands		
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YMQAVAREHGLYEHIRENTVSDAHWDESTORWKOLLYRDSGGOTQVDSNVVFAVGOL NRPMPAIPGIEFKGFPMFSAQMDHVDWMSGRKGVIGTGASATQIPOLAQTAARL KVFARTTWLLFTDLHEKISDSCKWLLAHVPHYSLWRYVMAMPQSVGFEDVMVDV GYPTELAVSARNDRLRQDISAMWEPQFADRPDLREVLIPDSPVGGKRIVRDNGTWLS TLKRDNVSMIRQPIEVITPKGICCVDCDTEHFDLIVYGTGFHASKFLMPINVTGRDGY ALHDVWKGDDARAVLGMTVQFPMNFWGPGTGLVYVSTVQFSEMTASTYVDAVRL LLEGHOSMEVKTPEVFESYINQVRVDEGNALRWGFSKVSWSYKNSKGRVTQNFPTAVE FQWTHSVEPTDYQLG"	2100 bp	mRNA linear	VRT 28-JUN-2004
AY189696			
LOCUS	Bothrops jararaca follicle-stimulating hormone receptor mRNA, complete cds.		
DEFINITION	Bothrops jararaca		
ACCESSION	AY189696		
VERSION	AY189696.1	GI:37778924	
KEYWORDS	Bothrops jararaca (jararaca)		
SOURCE	Bothrops jararaca		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.		
REFERENCE	1 (bases 1 to 2100)		
AUTHORS	Bluhm, A.P., Toledo, R.A., Mesquita, F.M., Pimenta, M.T., Fernandes, F.M., Ribela, M.T. and Lazari, M.F.		
TITLE	Molecular cloning, sequence analysis and expression of the snake follicle-stimulating hormone receptor		
JOURNAL	Gen. Comp. Endocrinol. 137 (3), 300-311 (2004)		
PUBMED	15201068		
REFERENCE	2 (bases 1 to 2100)		
AUTHORS	Bluhm, A.P.C., Mesquita, F.M. and Lazari, M.F.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (30-NOV-2002) Pharmacology, Federal University of Sao Paulo (UNIFESP), Rua Tres de Maio, 100, Sao Paulo, SP 04044-020, Brazil		
FEATURES	Location/Qualifiers		
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Query Match	91.1%;	Score 16.4;	DB 5; Length 2100;
Best Local Similarity	94.4%;	Pred. No. 3.6e+02;	
Matches	17; Conservative	0; Mismatches	1; Indels 0; Gaps 0;

1 ATGCTTGTTAGTGGCTG 18  
 738 ATGCTTGTTAGTGGCTG 721

BC060419 2735 bp mRNA linear VRT 03-FEB-2004  
 XENOPUS LAEVIS hypothetical protein MGC68664, mRNA (cDNA clone  
 MGC:68664 IMAGE:4032804), complete cds.

BC060419.1 GI:38014521  
 MGC.  
 XENOPUS LAEVIS (African clawed frog)  
 XENOPUS LAEVIS  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 Xenopodinae; Xenopus; Xenopus.

1 (bases 1 to 2735)  
 Klein, S.L., Strausberg, R.L., Wagner, L., Pontius, J., Clifton, S.W.  
 and Richardson, P.  
 Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 initiative  
 Dev. Dyn. 225 (4), 384-391 (2002)

12454917  
 2 (bases 1 to 2735)  
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
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 Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932  
 3 (bases 1 to 2735)  
 Klein, S. and Strausberg, R.  
 Direct Submission  
 Submitted (27-OCT-2003) National Institutes of Health, Xenopus Gene  
 Collection (XGC), National Institute of Child Health and Human  
 Development, 6100 Executive Boulevard, Room 4801, Rockville, MD  
 20892-7510, USA  
 NIH-MGC Project  
 Contact: XGC help desk  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Dr. Igor David  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC),  
 Gaithersburg, Maryland  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: nisc\_mgc@nhgri.nih.gov  
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
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 phosphate and teichoic acids"  
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RESULT 13  
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 DEFINITION  
 ACCESSION  
 VERSION  
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 Drosophila sp.  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

REMARK  
 COMMENT



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REFERENCE
AUTHORS      Venter, J.C., Adams, M., Li, P.W. and Myers, B.W.
TITLE        Detection kits, such as nucleic acid arrays, for detecting the
              expression of 10,000 or more Drosophila genes and uses thereof
JOURNAL      Patent: WO 017042-A 6676 27-SEP-2001;
              PE Corporation (NY) (US)
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Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 14
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DEFINITION    Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***.
ACCESSION     AC019883
VERSION       AC019883.1 GI:6665014
KEYWORDS      HTG; HTGS PHASE2.
SOURCE        Drosophila melanogaster (fruit fly)
ORGANISM      Drosophila melanogaster
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              Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
              Ephydroidea; Drosophilidae; Drosophila.
              1 (bases 1 to 17997)
REFERENCE     Adams, M. and Venter, J.C.
AUTHORS       Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
TITLE         Rockville, MD, USA
JOURNAL       This sequence was identified as CDM:10211264 by the submitter.
              For more information on this record e-mail to fly@celera.com.
              * NOTE: this is a 'working draft' sequence.
              * This sequence will be replaced
              * by the finished sequence as soon as it is available and
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DEFINITION    Human DNA sequence from clone RP11-642C7 on chromosome X, complete
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ACCESSION     AL845315
VERSION       AL845315.3 GI:22449829
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SOURCE        Homo sapiens (human)
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REFERENCE
AUTHORS      Whitehead, S.
TITLE        Direct Submission
JOURNAL      Submitted (20-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
              Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
              humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
              On Aug 22, 2002 this sequence version replaced gi:22416240.
              ----- Genome Center
              Center: Wellcome Trust Sanger Institute
              Center code: SC
              Web site: http://www.sanger.ac.uk
              Contact: humquery@sanger.ac.uk
              -----
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em, EMBL; Sw,
SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome X, constructed by the Sanger Centre Chromosome X Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/ChrX
RP11-642C7 is from the library RPCI-11.3 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
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Best Local Similarity 94.4%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION    Homo sapiens chromosome 15 clone RP11-113M15 map 15, LOW-PASS
              SEQUENCE SAMPLING.
ACCESSION     AC123988
VERSION       AC123988.1 GI:212327531
KEYWORDS      HTG; HTGS_PHASE0.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 58294)
REFERENCE     Birren, B., Linton, L., Nusbaum, C. and Lander, E.
AUTHORS

```

TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Homo sapiens chromosome 15, clone RP11-113M15  
2 (bases 1 to 58294)  
Birken, B., Linton, L., Nusbaum, C., Lander, E., Allen, N.,  
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Direct Submission  
Submitted (06-JUN-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center -----  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WBK  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information -----  
Center project name: L27313  
Center clone name: 113\_M\_15  
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\* NOTE: This record contains 71 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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4037 4136: gap of 100 bp  
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\* 9100 9831: contig of 732 bp in length  
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TITLE  
JOURNAL  
COMMENT

[illegible]

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## Query Match

91.1%; Score 16.4; DB 2; Length 70663;

Best Local Similarity 94.4%; Pred. No. 2.7e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGACTTGCTG 18

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## RESULT 18

AC010499/c

LOCUS

AC010499 Homo sapiens chromosome 5 clone CTD-236605, complete sequence.

DEFINITION

AC010499

VERSION

AC010499.6 GI:15887282

KEYWORDS

HTG.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 74377)

AUTHORS

DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE

Direct Submission

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 74377)

AUTHORS

DOE Joint Genome Institute.

TITLE

Direct Submission

JOURNAL

Submitted (15-SEP-1999)

REFERENCE

3 (bases 1 to 74377)

AUTHORS

DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE

Direct Submission

JOURNAL

Submitted (27-SEP-2000)

REFERENCE

4 (bases 1 to 74377)

AUTHORS

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TITLE

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TITLE

Direct Submission

JOURNAL

Submitted (27-SEP-2000)

REFERENCE

4 (bases 1 to 74377)

AUTHORS

DOE Joint Genome Institute and



\* 30588 30687: gap of 100 bp  
\* 30688 31615: contig of 928 bp in length  
\* 31616 31715: gap of 100 bp  
\* 31716 32500: contig of 935 bp in length  
\* 32501 32750: gap of 100 bp  
\* 32751 33680: contig of 930 bp in length  
\* 33681 33780: gap of 100 bp  
\* 33781 34707: contig of 927 bp in length  
\* 34708 34807: gap of 100 bp  
\* 34808 35881: contig of 974 bp in length  
\* 35882 35881: gap of 100 bp  
\* 35883 36784: contig of 903 bp in length  
\* 36785 36884: gap of 100 bp  
\* 36885 37813: contig of 929 bp in length  
\* 37814 37914: gap of 100 bp  
\* 37915 38655: contig of 952 bp in length  
\* 38656 39260: gap of 100 bp  
\* 39261 39920: contig of 955 bp in length  
\* 39921 40020: gap of 100 bp  
\* 40021 40937: contig of 917 bp in length  
\* 40938 41037: gap of 100 bp  
\* 41038 41980: contig of 943 bp in length  
\* 41981 42080: gap of 100 bp  
\* 42081 42997: contig of 917 bp in length  
\* 42998 43097: gap of 100 bp  
\* 43098 43997: contig of 900 bp in length  
\* 43998 44097: gap of 100 bp  
\* 44098 45007: contig of 910 bp in length  
\* 45008 45107: gap of 100 bp  
\* 45108 46068: contig of 981 bp in length  
\* 46069 46168: gap of 100 bp  
\* 46169 47090: contig of 922 bp in length  
\* 47091 47190: gap of 100 bp  
\* 47191 48084: contig of 894 bp in length  
\* 48085 48184: gap of 100 bp  
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\* 63506 63605: gap of 100 bp  
\* 63606 64553: contig of 948 bp in length  
\* 64554 65605: gap of 100 bp  
\* 65606 65705: contig of 952 bp in length  
\* 65706 66663: contig of 100 bp  
\* 66664 66763: gap of 100 bp  
\* 66764 67658: contig of 895 bp in length  
\* 67659 67759: gap of 100 bp

\* 67759 68638: contig of 880 bp in length  
\* 68639 68738: gap of 100 bp  
\* 68739 69643: contig of 905 bp in length  
\* 69644 69743: gap of 100 bp  
\* 69744 70691: contig of 948 bp in length  
\* 70692 70791: gap of 100 bp  
\* 70792 71697: contig of 906 bp in length  
\* 71698 71797: gap of 100 bp  
\* 71798 72708: contig of 911 bp in length  
\* 72709 72808: gap of 100 bp

Query Match 91.1%; Score 16.4; DB 2: Length 93330;  
Best Local Similarity 94.4%; Pred. No. 2.6e-02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGGTACTGGCTG 18  
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Db 7244 ATGCTTGGTACTGGCTG 7261  
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RESULT 20  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source

AC005554  
Drosophila melanogaster, chromosome 2L, region 23C4-23D4, P1 clones  
DS02380 and DS06823, complete sequence.  
AC005554 AC003745 AC002736 AC002737 AC001790 AC002738 AC001791  
AC002739 AC002740 AC002741 AC002742 AC002743 AC002744 AC002745  
AC002746 AC003195 AC002747 AC001792 AC002748 AC002749 AC002750  
AC002751 AC004487  
AC005554.2 GI:4389506  
HTG.  
Drosophila melanogaster (fruit fly)  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 93375)  
Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,  
Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,  
Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,  
Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,  
Kim, E., Lee, B., Lewis, S., Li, P., Lomocan, M.A., Mazda, P.,  
Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S.,  
Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E.,  
Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and  
Rubin, G.M.  
Sequencing of Drosophila chromosome 2L, region 23C4-23D4  
Unpublished (1998)  
2 (bases 1 to 93375)  
Celniker, S.E., George, R.A., Galle, R.F., Hoskins, R.A.,  
Svirskas, R.R., Harris, N.L., Agbayani, A., Arcaina, T.T., Baxter, E.,  
Blazej, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E.,  
Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,  
Kim, S.H., Lee, B., Lomocan, M.A., Mak, J., Mazda, P., Mok, M.S.,  
Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S.,  
Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E.,  
Yee, A., Zhang, R., Zieran, L.L. and Rubin, G.M.  
Direct Submission  
Submitted (29-AUG-1998) Berkeley Drosophila Genome Project, MS  
64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road,  
Berkeley, CA 94720, US  
On Mar 11, 1999 this sequence version replaced gi:3492870.  
Sequence submitted by:  
Lawrence Berkeley National Laboratory, MS 64-121  
Berkeley, CA 94720  
For further information about this sequence, including its location  
and relationship to other sequences, please visit our sequence  
archive Web site (<http://www.fruitfly.org/sequence/>) or send email  
to [bdgp@fruitfly.berkeley.edu](mailto:bdgp@fruitfly.berkeley.edu).  
P1 library locations: 25-76, 72-7.  
Location/Qualifiers  
1. .93375

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/organism="Drosophila melanogaster"
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/notes="This sequence represents a contig constructed by merging the sequences of two P1 clones, DS02380 (D142) and DS06823 (D207). The sequence of DS02380 (AC003745) matches this sequence from bp 1 to bp 26119 of the contig; however, we have determined that DS02380 is a chimera and the remaining nucleotides in this clone derive from another site in the genome. DS06823 (D207) corresponds to bp 9214 to bp 93371 of the contig."

ORIGIN
Query Match          91.1%; Score 16.4; DB 3; Length 93375;
Best Local Similarity 94.4%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGTTACTGGCTG 18
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Db 18995 ATGCTTGTTACTGGCTG 18978

RESULT 21
LOCUS          AC024567          99338 bp      DNA      linear      PRI 08-JUN-2001
DEFINITION      Homo sapiens chromosome 5 clone CTD-216113, complete sequence.
ACCESSION      AC024567
VERSION        AC024567.6 GI:14329095
KEYWORDS        HTG.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 99338)
  Doe Joint Genome Institute and Stanford Human Genome Center.
  Direct Submission
  Unpublished
  2 (bases 1 to 99338)
  Doe Joint Genome Institute.
  Direct Submission
  Submitted (29-FEB-2000) Production Sequencing Facility, DOE Joint
  Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
  3 (bases 1 to 99338)
  Doe Joint Genome Institute and Stanford Human Genome Center.
  Direct Submission
  Submitted (01-MAY-2001) DOE Joint Genome Institute, 2800 Mitchell
  Drive, Walnut Creek, CA 94598, USA
  4 (bases 1 to 99338)
  Doe Joint Genome Institute and Stanford Human Genome Center.
  Direct Submission
  Submitted (08-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell
  Drive, Walnut Creek, CA 94598, USA
  On Jun 8, 2001 this sequence version replaced gi:13899411.
  Draft Sequence Produced by DOE Joint Genome Institute
  www.jgi.doe.gov
  Finishing Completed at Stanford Human Genome Center
  www.srhgc.stanford.edu
  Quality: Phrap Quality >=40 99.9% of Sequence;
  Estimated Total Number of Errors is 0.1.
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      /mol_type="Genomic DNA"
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ORIGIN
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Query Match          91.1%; Score 16.4; DB 9; Length 99338;
Best Local Similarity 94.4%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 22
LOCUS          AF188026          101456 bp      DNA      linear      PRI 28-JUN-2002
DEFINITION      Homo sapiens chromosome 8 clone CTD-2373L20 map 8q24.3, complete
sequence.
ACCESSION      AF188026
VERSION        AF188026.4 GI:21622698
KEYWORDS        HTG.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 101456)
  Taudien,S., Blechschmidt,K., Menzel,U., Polley,A., Reichwald,K.,
  Rump,A., Schilhabel,M.B., Schudy,A., Wen,G. and Rosenthal,A.
  Chromosome 8 genomic sequence
  Unpublished
  2 (bases 1 to 101456)
  Taudien,S., Wen,G.P., Schilhabel,M., Menzel,U., Jahn,N.,
  Baumgart,C., Dette,M. and Rosenthal,A.
  Direct Submission
  Submitted (09-SEP-1999) Genome Analysis, Institute of Molecular
  Biotechnology, Butenbergrasse 11, Jena 07745, Germany
  3 (bases 1 to 101456)
  Lagemann,D. and Platzer,M.
  Direct Submission
  Submitted (28-JUN-2002) Genome Analysis, Institute of Molecular
  Biotechnology, Butenbergrasse 11, Jena 07745, Germany
  On Jun 28, 2002 this sequence version replaced gi:14327848.
  ----- Genome Center
  Center: Institute of Molecular Biotechnology
  Center code: IMB
  Web site: http://genome.imb-jena.de/
  Contact: gscj-submit@genome.imb-jena.de
  ----- Project Information
  Center project name: H237
  Center clone name: CTD-2373L20
  ----- Summary Statistics
  Sequencing vector: pUC18; 100% of reads
  Chemistry: Dye-terminator Big Dye; 100% of reads
  Assembly program: Phrap; version 0.990329
  Consensus quality: 100609 bases at least Q40
  Consensus quality: 101211 bases at least Q30
  Consensus quality: 101322 bases at least Q20
  Quality coverage: 6.82x
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  This sequence was finished as follows unless otherwise noted: all
  regions were double stranded, sequenced with an alternate
  chemistry, or covered by high quality data (i.e., phred quality >=
  30); an attempt was made to resolve all sequencing problems, such
  as compressions and repeats; all regions were covered by at least
  one plasmid subclone or more than one pUC18 subclone; and the
  assembly was confirmed by restriction digest.
  -----
  Sequence Quality Assessment:
  This entry has been annotated with sequence quality
  estimates computed by the Phrap assembly program.
  All manually edited bases have been reduced to quality zero.
  Quality levels above 40 are expected to have less than
  1 error in 10,000 bp.
  Base-by-base quality values are not generally visible from the
  GenBank flat file format but are available as part
  of this entry's ASN.1 file.
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## Query Match

Best Local Similarity 91.1%; Score 16.4; DB 9; Length 101456;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 56224 ATGCTTGCTACTTAGCTG 56207





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repeat_region      /rpt_family="L2"

Query Match      91.1%; Score 16.4; DB 9; Length 101459;
Best Local Similarity 94.4; Pred.No.2.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ATGCTTGCTACTTCGGCTG 18
Db      45235 ATGCTTGCTACTTCGGCTG 45252

RESULT 24
AC022136/c
LOCUS
DEFINITION Homo sapiens chromosome 5 clone CTD-2221K22, WORKING DRAFT
SEQUENCE, 37 unordered pieces.

125145 bp DNA linear HTG 06-MAY-2000
AC022136
Homo sapiens chromosome 5 clone CTD-2221K22, WORKING DRAFT
SEQUENCE, 37 unordered pieces.

AC022136
VERSION AC022136.3 GI:7711710
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 125145)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 125145)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On May 6, 2000 this sequence version replaced gi:7239447.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 712675
Center clone name: CITB-HI_2221K22
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Summary Statistics
Consensus quality: 93614 bases at least Q40
Consensus quality: 109475 bases at least Q30
Consensus quality: 112774 bases at least Q20
Estimated insert size: 97000; pulse field gel estimation
Estimated insert size: 121545; sum-of-contigs estimation
Quality coverage: 5.83 in Q20 bases; pulse field gel estimation
Quality coverage: 4.65 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 37 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 2572: contig of 2572 bp in length
* 2573 2672: gap of unknown length
* 2673 4770: contig of 2098 bp in length
* 4771 4870: gap of unknown length
* 4871 7164: contig of 2294 bp in length
* 7165 7264: gap of unknown length
* 7265 9449: contig of 2185 bp in length
* 9450 9549: gap of unknown length
* 9550 12367: contig of 2818 bp in length
* 12368 12467: gap of unknown length
* 12468 14902: contig of 2435 bp in length
* 14903 15002: gap of unknown length
* 15003 17643: contig of 2641 bp in length
* 17644 17743: gap of unknown length
* 17744 20541: contig of 2798 bp in length
* 20542 20641: gap of unknown length
* 20642 22879: contig of 2238 bp in length
* 22880 22979: gap of unknown length
* 22980 25050: contig of 2071 bp in length
* 25051 25150: gap of unknown length
* 25151 27710: contig of 2560 bp in length
* 27711 27810: gap of unknown length
* 27811 30269: contig of 2459 bp in length
* 30270 30370: gap of unknown length
* 30371 32585: contig of 2215 bp in length
* 32586 32685: gap of unknown length
* 32686 35719: contig of 3035 bp in length
* 35720 35819: gap of unknown length
* 35820 38323: contig of 2504 bp in length
* 38324 41441: gap of unknown length
* 41442 41441: contig of 3018 bp in length.
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* 41442 41541: gap of unknown length
* 41542 44320: contig of 2779 bp in length
* 44321 44420: gap of unknown length
* 44421 47540: contig of 3120 bp in length
* 47541 47640: gap of unknown length
* 47641 49266: contig of 2286 bp in length
* 49267 50026: gap of unknown length
* 50027 52948: contig of 2922 bp in length
* 52949 53048: gap of unknown length
* 53049 55892: contig of 2834 bp in length
* 55893 55982: gap of unknown length
* 55983 59431: contig of 3449 bp in length
* 59432 59531: gap of unknown length
* 59532 62545: contig of 3014 bp in length
* 62546 62645: gap of unknown length
* 62646 65729: contig of 3084 bp in length
* 65730 65829: gap of unknown length
* 65830 69494: contig of 3665 bp in length
* 69495 73557: gap of unknown length
* 73558 76848: contig of 3291 bp in length
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* 81441 84403: contig of 2861 bp in length
* 84404 84501: gap of unknown length
* 84502 87615: contig of 3114 bp in length
* 87616 90814: contig of 3099 bp in length
* 90815 90914: gap of unknown length
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* 94883 99188: contig of 4206 bp in length
* 99189 99288: gap of unknown length
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FEATURES             Location/Qualifiers
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        db_xref="taxon:9606"
        chromosome="5"
        clone="CTD-2221K22"
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ORIGIN
Query Match          91.1%; Score 16.4; DB 2; Length 125145;
Best Local Similarity 94.4%; Pred. No.2.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGCTTGCTACTGCTG 18
Db 37268 ATGCTTGCTACTGCTG 37251
RESULT 25
AC101834/c          135427 bp DNA linear ROD 01-JUL-2004
LOCUS              Mus musculus chromosome 15, clone RP24-497017, complete sequence.
DEFINITION
ACCESSION          AC101834
VERSION            AC101834.8 GI:49533860
KEYWORDS           HTG.
SOURCE             Mus musculus (house mouse)
ORGANISM           Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE          1 (bases 1 to 135427)
```

AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Birren, B., Nusbaum, C. and Lander, E.  
Mus musculus chromosome 15, clone RP24-497017  
2 (bases 1 to 135427)  
Unpublished  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,  
Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,  
Brown, A., Camarata, J., Campiano, A., Chang, J., Chazaro, B.,  
Choe, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,  
Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S.,  
Ferreira, P., Fitzhugh, W., Gage, D., Galsgan, J., Gardyna, S.,  
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,  
Hagos, B., Hesford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,  
Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,  
Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,  
Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,  
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrum, J.,  
Meneus, L., Mihova, T., Mieng, A., O'Connor, T., O'Donnell, P., O'Neill, D.,  
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,  
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,  
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R.,  
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,  
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,  
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA

TITLE  
JOURNAL  
REFERENCE  
AUTHORS

3 (bases 1 to 135427)  
Unpublished  
Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,  
Anderson, M., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V.,  
Bloom, T., Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J.,  
Choe, Y., Collymore, A., Cook, A., Cooke, P., Corum, B.,  
Dearellano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L.,  
Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D.,  
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Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Liu, X., Mabbitt, R.,  
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McCarthy, M., Meldrum, J., Meneus, L., Mihova, T., Mieng, A.,  
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Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, J., Raymond, C.,  
Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupack, R.,  
Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,  
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Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R.,  
Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L.,  
Zimmer, A. and Zody, M.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Direct Submission  
Submitted (01-MAY-2004) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
4 (bases 1 to 135427)  
Unpublished  
Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,  
Anderson, M., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V.,  
Bloom, T., Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J.,  
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Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Liu, X., Mabbitt, R.,  
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Zimmer, A. and Zody, M.

Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R.,  
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Zimmer, A. and Zody, M.

# TITLE JOURNAL

Submitted (01-JUN-2004) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jul 1, 2004 this sequence version replaced gi:46931442.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/MIT Center for Genome Research

Center code: WIKR

Web site: http://www-seq.wi.mit.edu

Contact: sequence\_submissions@broad.mit.edu

----- Project Information

Center project name: L17503

Center clone name: 497\_O\_17

## FEATURES source

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Best Local Similarity 94.4%; Fred. No. 2.5e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTGGCTG 18

Db 53212 ATGCTTGCTACTGGCTG 53195

## RESULT 26

AC149958

LOCUS

DEFINITION

Strongylocentrotus purpuratus clone R3-32B10, WORKING DRAFT

SEQUENCE, 10 unordered pieces.

AC149958

ACCESSION

AC149958.1 GI:49405924

VERSION

HTG; HTGS PHASE1; HTGS DRAFT.

KEYWORDS

Strongylocentrotus purpuratus

SOURCE

ORGANISM

Strongylocentrotus purpuratus

Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;

Echinoidea; Euechinoidea; Echinacea; Echinocida;

Strongylocentrotidae; Strongylocentrotus.

1 (bases 1 to 142071)

REFERENCE

AUTHORS

Muzny, D.M., Adams, C., Ali-Osman, F.R., Allen, C.,

Alsbrooks, S.L., Amarutunge, H.C., Are, J.R., Ayele, M., Banks, T.,

Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.,

Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,

Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,

Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Haviak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, K., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newtson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Picken, R., Primus, E., Fu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojebokan, I., Rolfe, M., Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Umani, K., Vasquez, L., Vera, V., Villalob, B., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watling, S., Williams, G., Williamson, A., Wleczyk, R., Woodson, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.

Direct Submission  
Unpublished  
2 (bases 1 to 142071)  
Worley, K.C.  
Direct Submission  
Submitted (29-JUN-2004) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
-----  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
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Project Information  
Center project name: SPON  
Center clone name: R3-32B10  
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Summary Statistics  
Sequencing vector: Plasmid  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 135191 bases at least Q40  
Consensus quality: 136821 bases at least Q30  
Consensus quality: 137832 bases at least Q20  
Estimated insert size: 147150; sum-of-contigs estimation  
Estimated insert size: 142071; agarose-fp estimation  
Quality coverage: 4x in Q20 bases; agarose-fp estimation  
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation  
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NOTE: Estimated insert size may differ from sequence length (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

2305: contig of 2305 bp in length  
2405: gap of unknown length  
4662: contig of 2257 bp in length  
4762: gap of unknown length  
8635: contig of 3773 bp in length  
8635: gap of unknown length  
13994: contig of 4359 bp in length  
13994: gap of unknown length  
21984: contig of 8890 bp in length  
21984: gap of unknown length  
22084: gap of unknown length  
37547: contig of 15463 bp in length  
37547: gap of unknown length  
52705: contig of 15058 bp in length  
52705: gap of unknown length  
52805: gap of unknown length  
74984: contig of 22179 bp in length  
74984: gap of unknown length  
75085: 105312: contig of 30228 bp in length  
105313 105412: gap of unknown length  
142071: contig of 36659 bp in length.  
Location/Qualifiers  
1..142071  
/organism="Strongylocentrotus purpuratus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7668"  
/clone="R3-32B10"  
  
Query Match 91.1%; Score 16.4; DB 2; Length 142071;  
Best Local Similarity 94.4%; Pred. NO. 2.5e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 ATGCTTGCTACTTGCTG 18  
Db 89226 ATGCTTGCTACTTGCTG 89243  
  
FEATURES  
source  
ORIGIN  
Query Match 91.1%; Score 16.4; DB 2; Length 142071;  
Best Local Similarity 94.4%; Pred. NO. 2.5e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
RESULT 27  
AL808021/c 149561 bp DNA linear ROD 21-JAN-2003  
LOCUS Mouse DNA sequence from clone RP23-349B15 on chromosome 11,  
DEFINITION complete sequence.  
ACCESSION AL808021  
VERSION AL808021.12 GI:27817345  
KEYWORDS HTG.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Dunn, M.  
Direct Submission  
Submitted (21-JAN-2003) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
[humquerry@sanger.ac.uk](mailto:humquerry@sanger.ac.uk) Clone requests: [clonerequest@sanger.ac.uk](mailto:clonerequest@sanger.ac.uk)  
On Jan 21, 2003 this sequence version replaced gi:27550983.  
Sequence from the Mouse Genome Sequencing Consortium whole genome  
shotgun may have been used to confirm this sequence. Sequence data  
from the whole genome shotgun alone has only been used where it has  
a phred quality of at least 30.  
-----  
Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: [humquerry@sanger.ac.uk](mailto:humquerry@sanger.ac.uk)  
-----  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all  
regions were either double-stranded or sequenced with an alternate

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WormPEP; Information on the WormPEP database can be found at

[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) RP23-349B15 is from the RPCI-23 Mouse BAC Library

constructed by the group of Pieter de Jong.

For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBAC3.6

## FEATURES

source

Location/Qualifiers

1..149561  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/chromosome="11"  
/clone="RP23-349B15"  
/clone\_lib="RPCI-23"

## ORIGIN

Query Match 91.1%; Score 16.4; DB 10; Length 149561;  
Best Local Similarity 94.4%; Pred. No. 2.5e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 ATGCTTGCTACTTGCTG 18  
Db 145269 ATGCTTGCTACTTGCTG 145252

## RESULT 28

AC064820/C

LOCUS AC064820 156842 bp DNA linear HTG 07-JUL-2000  
DEFINITION Homo sapiens chromosome 10 clone RP11-113M14, WORKING DRAFT  
SEQUENCE, 32 unordered pieces.

## ACCESSION

AC064820

AC064820.3 GI:7770018

VERSION HTG; HTGS PHASE1; HTGS\_DRAFT.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Waterston,R.H.

The sequence of Homo sapiens clone

Unpublished

2 (bases 1 to 156842)

Waterston,R.H.

Direct Submission

Submitted (22-APR-2000) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

On May 11, 2000 this sequence version replaced gi:7709938.

## COMMENT

----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC

Web site:<http://genome.wustl.edu/gsc/index.shtml>

----- Project Information -----

Center project name: H\_NH0113M14

----- Summary Statistics -----

Sequencing vector: M13; 100%

Chemistry: Dye-primer ET; 100% of reads

Chemistry: Dye-terminator Big Dye; 0% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 136221 bases at least Q40

Consensus quality: 142808 bases at least Q30

Consensus quality: 145854 bases at least Q20

Insert size: 181000; agarose-fp  
Insert size: 153742; sum-of-contigs  
Quality coverage: 3.01 in Q20 bases; agarose-fp  
Quality coverage: 3.67 in Q20 bases; sum-of-contigs  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 32 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1061: contig of 1061 bp in length  
\* 1062 1161: gap of unknown length  
\* 1162 3372: contig of 2211 bp in length  
\* 3373 3472: gap of unknown length  
\* 3473 5623: contig of 2151 bp in length  
\* 5624 8044: gap of unknown length  
\* 8045 8144: gap of unknown length  
\* 8145 10448: contig of 2304 bp in length  
\* 10449 10548: gap of unknown length  
\* 10549 12930: contig of 2382 bp in length  
\* 12931 13030: gap of unknown length  
\* 13031 15909: contig of 2879 bp in length  
\* 15910 16009: gap of unknown length  
\* 16010 18586: contig of 2977 bp in length  
\* 18587 19086: gap of unknown length  
\* 19087 21628: contig of 2542 bp in length  
\* 21629 21728: gap of unknown length  
\* 21729 24297: contig of 2569 bp in length  
\* 24298 24397: gap of unknown length  
\* 24398 26971: contig of 2574 bp in length  
\* 26972 27071: gap of unknown length  
\* 27072 29168: contig of 2097 bp in length  
\* 29169 29268: gap of unknown length  
\* 29269 33116: contig of 3848 bp in length  
\* 33117 33216: gap of unknown length  
\* 33217 36265: contig of 3049 bp in length  
\* 36266 36365: gap of unknown length  
\* 36366 40455: contig of 4090 bp in length  
\* 40456 48555: gap of unknown length  
\* 48556 43976: contig of 3421 bp in length  
\* 43977 44076: gap of unknown length  
\* 44077 48471: contig of 4395 bp in length  
\* 48472 48571: gap of unknown length  
\* 48572 54120: contig of 5549 bp in length  
\* 54121 54220: gap of unknown length  
\* 54221 59304: contig of 5084 bp in length  
\* 59305 59404: gap of unknown length  
\* 59405 66114: contig of 6710 bp in length  
\* 66115 66214: gap of unknown length  
\* 66215 70801: contig of 4587 bp in length  
\* 70802 70901: gap of unknown length  
\* 70902 76493: contig of 5592 bp in length  
\* 76494 76593: gap of unknown length  
\* 76594 81502: contig of 4909 bp in length  
\* 81503 81602: gap of unknown length  
\* 81603 86593: contig of 4991 bp in length  
\* 86594 93482: gap of unknown length  
\* 93483 93582: gap of unknown length  
\* 93583 100360: contig of 6778 bp in length  
\* 100361 100460: gap of unknown length  
\* 100461 107515: contig of 7055 bp in length  
\* 107516 107615: gap of unknown length  
\* 107616 114416: contig of 6801 bp in length  
\* 114417 114516: gap of unknown length  
\* 114517 121788: contig of 7272 bp in length  
\* 121789 121888: gap of unknown length  
\* 121889 131066: contig of 9178 bp in length  
\* 131067 131166: gap of unknown length

\* 131167 144496: contig of 13330 bp in length  
 \* 144497 144596: gap of unknown length  
 \* 144597 156842: contig of 12246 bp in length.

## FEATURES

## source

Location/Qualifiers  
 1. .156842  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="10"  
 /clone="RP11-113M14"  
 1. .1061

## misc\_feature

/note="assembly\_name:Contig42"  
 1162. .3372

## misc\_feature

/note="assembly\_name:Contig43"  
 3473. .5623

## misc\_feature

/note="assembly\_name:Contig44"  
 5724. .8044

## misc\_feature

/note="assembly\_name:Contig45"  
 8145. .10448

## misc\_feature

/note="assembly\_name:Contig46"  
 10549. .12930

## misc\_feature

/note="assembly\_name:Contig47"  
 13031. .15909

## misc\_feature

/note="assembly\_name:Contig48"  
 16010. .18986

## misc\_feature

/note="assembly\_name:Contig49"  
 19087. .21628

## misc\_feature

/note="assembly\_name:Contig50"  
 21729. .24297

## misc\_feature

/note="assembly\_name:Contig51"  
 24398. .26971

## misc\_feature

/note="assembly\_name:Contig52"  
 27072. .29168

## misc\_feature

/note="assembly\_name:Contig53"  
 29269. .33116

## misc\_feature

/note="assembly\_name:Contig54"  
 33217. .36265

## misc\_feature

/note="assembly\_name:Contig55"  
 36366. .40455

## misc\_feature

/note="assembly\_name:Contig56"  
 40556. .43976

## misc\_feature

/note="assembly\_name:Contig57"  
 44077. .48471

## misc\_feature

/note="assembly\_name:Contig58"  
 48572. .54120

## misc\_feature

/note="assembly\_name:Contig59"  
 54221. .59304

## misc\_feature

/note="assembly\_name:Contig60"  
 59405. .66114

## misc\_feature

/note="assembly\_name:Contig61"  
 66215. .70801

## misc\_feature

/note="assembly\_name:Contig62"  
 70902. .76493

## misc\_feature

/note="assembly\_name:Contig63"  
 76594. .81502

## misc\_feature

/note="assembly\_name:Contig64"  
 clone\_end:sp6  
 vector\_side:left"

## misc\_feature

81603. .86593  
 /note="assembly\_name:Contig65"

## misc\_feature

86694. .93482  
 /note="assembly\_name:Contig66"

## misc\_feature

93583. .100360  
 /note="assembly\_name:Contig67"

## misc\_feature

100461. .107515  
 /note="assembly\_name:Contig68"

## misc\_feature

107616. .114416  
 /note="assembly\_name:Contig69"

## misc\_feature

114517. .121788  
 /note="assembly\_name:Contig70"

## misc\_feature

121889. .131066  
 /note="assembly\_name:Contig71"

## misc\_feature

131167. .144496

/note="assembly\_name:Contig72"  
 clone\_end:r7  
 vector\_side:left"  
 144597. .156842  
 /note="assembly\_name:Contig73"

## misc\_feature

## ORIGIN

Query Match 91.1%; Score 16.4; DB 2; Length 156842;  
 Best Local Similarity 94.4%; Pred.No. 2.5e+00;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTTGCTG 18

Db 103813 ATGCTTAGTACTTGCTG 103796

## RESULT 29

AC092187

## LOCUS

AC092187 164920 bp DNA linear INV 31-JUL-2004

## DEFINITION

Drosophila melanogaster clone BACR23N06, complete sequence.

## ACCESSION

AC092187.2 GI:50872295

## VERSION

HTG.

## KEYWORDS

Drosophila melanogaster (fruit fly)

## SOURCE

Drosophila melanogaster

## ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

## REFERENCE

1 (bases 1 to 164920)

## AUTHORS

Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banazon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorset, V., Dou, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houch, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Neilson, K.A., Nunoo, J., Pacieb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.

## TITLE

Submitted (26-JUN-2001) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US

## REFERENCE

2 (bases 1 to 164920)

## AUTHORS

Celniker, S., Carlson, J., Wan, K., Pfeiffer, B., Frise, E., George, R., Hoskins, R., Stapleton, M., Pacieb, J., Park, S., Svirskas, R., Smith, E., Yu, C. and Rubin, G.

## TITLE

Submitted (31-JUL-2004) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US

## COMMENT

Sequence submitted by:  
 Berkeley Drosophila Genome Project  
 Lawrence Berkeley National Laboratory  
 Berkeley, CA 94720

This sequence submission incorporates changes made during reevaluation of the assembly or fingerprint verification of the clone. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site <http://www.fruitfly.org/sequence/> or send email to [bdgp@fruitfly.org](mailto:bdgp@fruitfly.org).

## FEATURES

## source

Location/Qualifiers  
 1. .164920  
 /organism="Drosophila melanogaster"  
 /mol\_type="genomic DNA"  
 /strain="y; cn bw sp"  
 /db\_xref="taxon:7227"  
 /chromosome="2L"  
 /map="23E-23F"

/clone="BAC clone BACR22N06 (D1291)"  
 /clone\_lib="RPC1-99 (Roswell Park Cancer Institute  
 Drosophila melanogaster BAC library, partial EcoRI in  
 pBACe3.6)"

## ORIGIN

Query Match 91.1%; Score 16.4; DB 3; Length 164920;  
 Best Local Similarity 94.4%; Pred. No. 2.5e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTTGCTG 18

|||||

Db 6374 ATGCTTGCTACTTGCTG 6391

## RESULT 30

HSBA80K6/c

LOCUS

DEFINITION

Human DNA sequence from clone RP11-80K6 on chromosome 20 Contains a putative novel gene, an RPL36 (60S ribosomal protein L36)

Pseudogene, ESTs, STSs, GSSs and a CpG island, complete sequence.

ACCESSION

AL121902.13 GI:7635633

KEYWORDS

HTG; CpG island; ribosomal protein; RPL36.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (21-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
 requests: clonerequest@sanger.ac.uk  
 On Apr 22, 2000 this sequence version replaced gi:7452953.  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 The following abbreviations are used to associate primary accession  
 numbers given in the feature table with their source databases:  
 Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information  
 on the WORMPEP database can be found at  
[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence  
 was generated from part of bacterial clone contigs of human  
 chromosome 20, constructed by the Sanger Centre Chromosome 20  
 Mapping Group. Further information can be found at  
<http://www.sanger.ac.uk/HGP/Chr20>  
 This sequence is the entire insert of clone RP11-80K6 The true left  
 end of clone RP5-91115 is at 81631 in this sequence. The true right  
 end of clone RP4-606D23 is at 63129 in this sequence. This sequence  
 was finished as follows unless otherwise noted: all regions were  
 either double-stranded or sequenced with an alternate chemistry or  
 covered by high quality data (i.e., phred quality >= 30); an  
 attempt was made to resolve all sequencing problems, such as  
 compressions and repeats; all regions were covered by at least one  
 plasmid subclone or more than one M13 subclone; and the assembly  
 was confirmed by restriction digest. RP11-80K6 is from the library  
 RPC1-11.1 constructed by the group of Pieter de Jong. For further  
 details see  
<http://www.chori.org/bacpac/home.htm>  
 VECTOR: pBACe3.6.  
 Location/Qualifiers  
 1..170740  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="20"  
 /clone="RP11-80K6"  
 /clone\_lib="RPC1-11.1"  
 misc\_feature 9..348

/note="match: GSS: Em:AQ214288"  
 58..365  
 /note="AluSq repeat: matches 1..308 of consensus"  
 2697..2793  
 /note="L2 repeat: matches 2584..2685 of consensus"  
 2852..2881  
 /note="10 copies 3 mer ttg 90% conserved"  
 2882..3183  
 /note="AluY repeat: matches 1..294 of consensus"  
 3582..3801  
 /note="MER20 repeat: matches 1..218 of consensus"  
 5137..5200  
 /note="L2 repeat: matches 2686..2750 of consensus"  
 5208..5394  
 /note="MER63A repeat: matches 1..200 of consensus"  
 5404..5627  
 /note="L2 repeat: matches 2435..2669 of consensus"  
 6114..6204  
 /note="MIR repeat: matches 48..140 of consensus"  
 6674..6850  
 /note="MIR repeat: matches 20..208 of consensus"  
 7231..7676  
 /note="match: GSS: Em:AQ110616"  
 7305..7613  
 /note="AluX repeat: matches 1..309 of consensus"  
 7820..8180  
 /note="THE1B repeat: matches 1..364 of consensus"  
 complement(8113..8485)  
 /note="match: GSS: Em:AQ005845"  
 8221..8421  
 /note="MER3 repeat: matches 2..207 of consensus"  
 8553..8783  
 /note="MIR repeat: matches 9..253 of consensus"  
 complement(8571..9123)  
 /note="match: GSS: Em:AQ535756"  
 complement(join(9444..9613,13673..13929))  
 /gene="bA80K6.1"  
 complement(join(<9444..9613,13673..>13929))  
 /gene="bA80K6.1"  
 /product="bA80K6.1 (putative novel transcript)"  
 /note="match: ESTs: Em:A1678044"  
 /evidence=not\_experimental  
 9584..9688  
 /note="MIR repeat: matches 51..154 of consensus"  
 9731..9920  
 /note="MER3 repeat: matches 1..209 of consensus"  
 complement(11089..11270)  
 /gene="bA80K6.1"  
 /note="match: STS: Em:G01521"  
 11602..11686  
 /note="L2 repeat: matches 2631..2710 of consensus"  
 12701..12796  
 /note="16 copies 6 mer atatat 68% conserved"  
 12705..12814  
 /note="5 copies 22 mer 70% conserved"  
 complement(12948..13482)  
 /gene="bA80K6.1"  
 /note="match: GSS: Em:AQ233886"  
 13129..13195  
 /note="MIR repeat: matches 190..256 of consensus"  
 13289..13305  
 /note="MIR repeat: matches 25..61 of consensus"  
 14423..14469  
 /note="MIR repeat: matches 85..130 of consensus"  
 14573..15011  
 /note="L1PA14 repeat: matches 5711..6149 of consensus"  
 15272..15463  
 /note="MIR repeat: matches 66..252 of consensus"  
 16366..16778  
 /note="match: GSS: Em:AQ713131"  
 16799..16886  
 /note="22 copies 4 mer gaga 76% conserved"  
 16800..16889



```

/note="15 copies 6 mer agagag 75% conserved"
19224..19374
/note="L2 repeat: matches 2539. .2704 of consensus"
repeat_region
19389..19430
/note="Charlie4a repeat: matches 36. .76 of consensus"
repeat_region
19431..19743
/note="AluY repeat: matches 1. .309 of consensus"
repeat_region
19744..20098
/note="Charlie4a repeat: matches 76. .439 of consensus"
repeat_region
20739..20786
/note="12 copies 4 mer caca 87% conserved"
repeat_region
20740..20785
/note="23 copies 2 mer ac 89% conserved"
repeat_region
20752..20787
/note="6 copies 6 mer acacac 97% conserved"
repeat_region
20794..21401
/note="MER82 repeat: matches 52. .652 of consensus"
repeat_region
21409..21709
/note="MUT2E repeat: matches 3. .314 of consensus"
repeat_region
22304..22382
/note="MER58 repeat: matches 2215. .2293 of consensus"
repeat_region
22402..22643
/note="MUR1J repeat: matches 112. .371 of consensus"
repeat_region
23107..23172
/note="3 copies 22 mer 83% conserved"
repeat_region
23109..23170
/note="31 copies 2 mer ac 82% conserved"
repeat_region
23123..23170
/note="8 copies 6 mer acacac 89% conserved"
misc_feature
complement(23705..24169)
/note="match: GSS: Em:AQ515387"
repeat_region
24527..24572
/note="2 copies 23 mer 100% conserved"
repeat_region
25692..25997
/note="MER58B repeat: matches 2. .341 of consensus"
repeat_region
27028..27115
/note="4 copies 22 mer 73% conserved"
repeat_region
27030..27093
/note="16 copies 4 mer agag 78% conserved"
repeat_region
27490..27731
/note="L1P4A repeat: matches 5566. .5805 of consensus"
repeat_region
27732..28078
/note="L1P4A repeat: matches 5798. .6144 of consensus"
repeat_region
29220..29326
/note="MER58 repeat: matches 5. .128 of consensus"
repeat_region
29362..29531
/note="L2 repeat: matches 2245. .2417 of consensus"
repeat_region
29589..29905
/note="MLR1C repeat: matches 187. .466 of consensus"
repeat_region
29906..30065
/note="AluYb repeat: matches 124. .288 of consensus"
repeat_region
30066..30327
/note="AluX repeat: matches 40. .296 of consensus"
repeat_region
30328..30452
/note="AluYb repeat: matches 1. .124 of consensus"
repeat_region
30453..30629
/note="MLR1C repeat: matches 1. .187 of consensus"
repeat_region
30702..30844
/note="L2 repeat: matches 2593. .2749 of consensus"
misc_feature
32132..32829
/note="match: GSS: Em:AQ381845"
repeat_region
32204..32423
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repeat_region
32991..33229
/note="L1ME repeat: matches 5419. .5661 of consensus"
repeat_region
33206..35037
/note="L1M4 repeat: matches 3203. .5031 of consensus"
repeat_region
35039..36782
/note="L1MBC repeat: matches 1119. .2557 of consensus"
repeat_region
36819..36956
/note="L1MBC repeat: matches 897. .1049 of consensus"

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Query Match 91.1%; Score 16.4; DB 9; Length 170740;

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Best Local Similarity 94.4%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGGTACTTGGCTG 18
DB 63056 ATGCTTGGTACTTGGCTG 63039

RESULT 31
AC125000 176597 bp DNA linear HTG 09-MAR-2004
MUS musculus chromosome 6 clone RP24-409L6 map 6, *** SEQUENCING IN
PROGRESS ***, 8 unordered pieces.
AC125000
AC125000.4 GI:45268815
HTG; HTGS PHASE1; HTGS FULLTOP; HTGS_ACTIVEFIN.
MUS musculus (house mouse)
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 176597)
Birren,B., Nusbaum,C. and Lander,E.
MUS musculus chromosome 6, clone RP24-409L6
Unpublished
2 (bases 1 to 176597)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,I., Boguslavsky,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collamore,A.,
Cook,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzgerald,M., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I.,
Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Larocque,K.,
Lamazares,R., Landers,T., Lehotzky,J., Levine,R., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N.,
Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meidrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C.,
Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (20-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 176597)
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavsky,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collamore,A., Cooke,A., Cooke,P., Corum,B., DeArelano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,X., Lui,A., Mabbitt,C., McCarthy,M.,
Macdonald,P., Major,J., Manning,J., Mlenga,T., Murphy,T., Naylor,J.,
Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., O'Donnell,P.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (09-MAR-2004) Whitehead Institute/MIT Center for Genome

```

## COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Mar 9, 2004 this sequence version replaced gi:29294292.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIGR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: 125636  
 Center clone name: 409\_L\_6

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 8 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\* 1 13262: contig of 13262 bp in length  
 \* 13263 13362: gap of 100 bp  
 \* 13363 17537: contig of 4175 bp in length  
 \* 17538 17637: gap of 100 bp  
 \* 17638 22133: contig of 4496 bp in length  
 \* 22134 22233: gap of 100 bp  
 \* 22234 69298: contig of 47065 bp in length  
 \* 69299 69393: gap of 100 bp  
 \* 69393 98285: contig of 28887 bp in length  
 \* 98286 98385: gap of 100 bp  
 \* 98386 128385: contig of 30000 bp in length  
 \* 128386 128485: gap of 100 bp  
 \* 128486 147341: contig of 18856 bp in length  
 \* 147342 147441: gap of 100 bp  
 \* 147442 176597: contig of 29156 bp in length.

FEATURES  
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 /db\_xref="taxon:10090"  
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 /clones="RP24-409L6"  
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## ORIGIN

Query Match 91.1%; Score 16.4; DB 2; Length 176597;  
 Best Local Similarity 94.4%; Pred. No. 2.5e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGCTACTGGCTG 18  
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 Db 40556 ATGCTTGCTACTGGCTG 40573

RESULT 32  
AL445237

LOCUS AL445237 182955 bp DNA linear PRI 09-MAY-2001  
 DEFINITION Human DNA sequence from clone RP13-238F13 on chromosome 10,  
 complete sequence.

## ACCESSION

AL445237

## VERSION

AL445237.16 GI:14018288

## KEYWORDS

HTG.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 182955)

## AUTHORS

Wilson, S.

## TITLE

Direct Submission

## JOURNAL

Submitted (09-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire,

## COMMENT

CB10 13A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone  
 requests: clonerequest@sanger.ac.uk  
 On May 11, 2001 this sequence version replaced gi:12709924.  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >=  
 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest. The following  
 abbreviations are used to associate primary accession numbers given  
 in the feature table with their source databases: Em, EMBL; Sw,  
 SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP  
 database can be found at

http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence  
 was generated from part of bacterial clone contigs of human  
 chromosome 10, constructed by the Sanger Centre Chromosome 10  
 Mapping Group. Further information can be found at  
 http://www.sanger.ac.uk/HGP/Chr10

RP13-238F13 is from the library RPCI-13.1 constructed by the group  
 of Pieter de Jong. For further details see  
 http://www.chori.org/bacpac/home.htm

VECTOR: pBAC3.6

This sequence is the entire insert of clone RP13-238F13 The true  
 left end of clone RP11-4507 is at 68195 in this sequence.

FEATURES  
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 /map="2424"

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repeat_region 10861. 10933
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repeat_region 11821. 11885
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repeat_region 14335. 14488
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repeat_region 31360. 31534
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repeat_region 32405. 32723
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repeat_region 32747. 33071
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repeat_region 33463. 33832
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repeat_region 34207. 34497
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Query Match 91.1%; Score 16.4; DB 9; Length 182955;  
Best Local Similarity 94.4%; Pred. No. 2.5e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTTGCTG 18

Db 124760 ATGCTTAGTACTTGCTG 124777

RESULT 33

AC099022

LOCUS

DEFINITION

AC099022

AC099022.1

HTG

AC099022

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AC099022 184554 bp DNA linear INV 08-NOV-2001  
Drosophila melanogaster, chromosome 2L, region 23C-23D, BAC clone  
BACR48B06, complete sequence.  
AC099022  
AC099022.1 GI:16798954  
HTG  
Drosophila melanogaster (fruit fly)  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 184554)  
Celtiker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,  
Kolt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,  
Rogers, J., An, H., Baldwin, D., Banazon, J., Benson, K.V., Busam, D.A.,  
Carlson, J.W., Center, A., Champs, M., Davenport, L.B., Dietz, S.M.,  
Dodson, K., Dorsett, V., Dou, L.E., Doyle, C., Dresnek, D., Farfan, D.,  
Fierliera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A.,  
Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,  
Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A.,  
McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J.,

Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B.,  
Phouanavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F.,  
Stapleton,M., Strong,R., Svirskaas,R., Tector,C., Williams,S.M.,  
Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.  
Sequencing of Drosophila chromosome 2L, region 23C-23D

# TITLE JOURNAL REFERENCE AUTHORS

2 (bases 1 to 184554)  
Celniker,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,  
Holt,R.A., Evans,C.A., Cocayne,J.D., Amanatides,P.G., Brandon,R.C.,  
Rogers,J., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A.,  
Carlson,K.W., Center,A., Champs,M., Davenport,L.B., Dietz,S.M.,  
Dodson,K., Dorset,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D.,  
Ferreira,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A.,  
Gonzalez,M., Hock,J., Hoskins,R.A., Hostin,D., Howland,T.J.,  
Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A.,  
McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J.,  
Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B.,  
Phouanavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F.,  
Stapleton,M., Strong,R., Svirskaas,R., Tector,C., Williams,S.M.,  
Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.  
Direct Submission

# TITLE JOURNAL

Submitted (08-NOV-2001) Berkeley Drosophila Genome Project, MS  
64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road,  
Berkeley, CA 94720, US

# COMMENT

Sequence submitted by:  
Berkeley Drosophila Genome Project  
Lawrence Berkeley National Laboratory, MS 64-121  
Berkeley, CA 94720

This sequence was assembled using end sequences from a whole genome  
shotgun and from subclones of this BAC and its neighboring clones.  
For further information about this sequence, including its location  
and relationship to other sequences, please visit our sequence  
archive Web site (<http://www.fruitfly.org/sequence/>) or send email  
to [bdgp@fruitfly.berkeley.edu](mailto:bdgp@fruitfly.berkeley.edu).

# FEATURES

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/mol\_type="genomic DNA"  
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/map="23C-23D"  
/clone="BACR48B06 (D1325)"  
/clone\_lib="RPCL-98 (Roswell Park Cancer Institute  
Drosophila melanogaster BAC library, partial EcoRI in  
pBACE3.6)"

# ORIGIN

Query Match 91.1%; Score 16.4; DB 3; Length 184554;  
Best Local Similarity 94.4%; Pred. No. 2.5e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTTGCTACTGCGTG 18

Db 157167 ATGCTTGCTACTGCGTG 157184

# RESULT 34

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LOCUS Homo sapiens 8 BAC RP11-709E21 (Roswell Park Cancer Institute Human  
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AC007860  
ACCESSION AC007860  
VERSION AC007860.6 GI:5649179  
KEYWORDS HYG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 186298)  
Muzny,D., Arenson,A.D., Bouck,J., Bunac,C., Chen,Z., Ding,Y.,  
Dugan,S., Durbin,J., Forcum,J., Garcia,C., Gorrell,J.H.,  
Corrall,L.L., Hernandez,J., Issar,A., Jackson,L., Kneitz,S.,

Kondejewski,N., Lau,S., Leal,B., Lee,B., Lichtarge,O., Liu,W.,  
Logan,O., Lu,J., Marondei,I., Martinez,C., Merscher,S., Miller,A.,  
Montgomery,K., Owall,G., Pampell,L.R., Parish,B.J., Perez,L.,  
Rashid,N.D., Rives,C., Scherer,S.E., Shen,H., Shim,C., Simon,M.,  
Vo,O., Williamson,A., Worley,K.C., Xhang,A.M., Yang,R., Yu,W.,  
Zhou,X., Kucherlapati,R., Nelson,D. and Gibbs,R.A.  
Direct Submission

# TITLE JOURNAL REFERENCE AUTHORS

2 (bases 1 to 186298)  
Worley,K.C.  
Direct Submission  
Submitted (18-JUN-1999) Molecular and Human Genetics, Baylor  
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

# REFERENCE AUTHORS

3 (bases 1 to 186298)  
Worley,K.C.

# TITLE JOURNAL

Submitted (29-JUL-1999) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

# REFERENCE AUTHORS

4 (bases 1 to 186298)  
Worley,K.C.  
Direct Submission  
Submitted (31-JUN-1999) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

# REFERENCE AUTHORS

5 (bases 1 to 186298)  
Worley,K.C.  
Direct Submission  
Submitted (09-OCT-1999) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

# REFERENCE AUTHORS

6 (bases 1 to 186298)  
Worley,K.C.  
Direct Submission  
Submitted (31-JAN-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Jul 29, 1999 this sequence version replaced gi:5542029.  
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email  
[gc-help@bcm.tmc.edu](mailto:gc-help@bcm.tmc.edu)

# COMMENT

CLONE LENGTH: This sequence does not necessarily represent the  
entire insert of this clone. Overlapping regions of clones are only  
sequenced and submitted once, so the sequence for the remainder of  
the insert may be found in the record for the adjacent clones.  
Overlapping clones are noted at the beginning and end of the  
Features listing.

# ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches  
of a local database that includes entries from dbSTS, GDB, and  
local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green,  
unpublished.) for Human and Mouse sequences.  
Genes and Region of sequence similarity are identified by BLAST  
(Nuc. Acids Res 25:3389-3402) similarity (expect < 1e-34) to the  
EST and cDNA sequences. Genes demonstrate at least two exons  
flanked by consensus splice sites that maintained sequence  
continuity across the splice junctions. Sequences that are not  
identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum  
standard of double strand coverage with a minimum of 2 clones and 2  
reads with no ambiguities or 2 chemistries with a minimum of 2  
clones and 3 reads with no ambiguities. If the sequence quality for  
a region does not meet this standard, it will be indicated in the  
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality  
standards - estimated error rate less than 1 per 10,000 bases.  
Reports of lowest quality individual bases and measures of base  
quality are listed below. Description of the metrics can be found  
at URL:

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 196314)

REFERENCE

AUTHORS

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,  
Alsbrooks, S.L., Amarutunge, H.C., Are, J.R., Ayelle, M., Banks, T.,  
Barbarta, J., Benton, J., Biemage, K., Blankenburg, K., Bonnin, D.,  
Bouck, J., Bowie, S., Brieva, M., Brown, M., Brown, N.P., Bryant, N.P.,  
Buahy, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,  
Carson, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,  
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,  
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,  
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,  
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,

Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,  
 Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,  
 Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,  
 Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,  
 Gorrell, J.H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, K.,  
 Harris, K., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,  
 Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,  
 Homai, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,  
 Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,  
 Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,  
 Kratovic, J., Kurashi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,  
 Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseg, H.,  
 Lozada, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,  
 Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,  
 Massey, E., Mahoney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,  
 Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,  
 Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,  
 Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G.,  
 Oreguene, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,  
 Peters, L., Pickens, R., Primus, E., Pu, L.B., Quiles, M., Ren, Y.,  
 Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G.,  
 Scherer, S., Scott, G., Shen, H., Shoohtari, N., Sisson, I.,  
 Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,  
 Sutton, A., Svatek, A., Taber, P., Tamerisa, A., Tamerisa, K., Tang, H.,  
 Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,  
 Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,  
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,  
 Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,  
 Wu, C., Wu, Y., Zhou, J., Zorrilla, S., Nelson, D.,  
 Weinstein, G. and Gibbs, R.

Direct Submission  
 Unpublished  
 2 (bases 1 to 186314)  
 Worley, K.C.

Direct Submission  
 Submitted (14-JAN-2000) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 186314)  
 Worley, K.C.

Direct Submission  
 Submitted (12-NOV-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Nov 12, 2002 this sequence version replaced gi:19172824.

----- Genome Center -----  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
 ----- Project Information -----  
 Center project name: HMKZ  
 Center clone name: RP11-709E21A  
 ----- Summary Statistics -----  
 Sequencing vector: M13;  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 180847 bases at least Q40  
 Consensus quality: 182651 bases at least Q30  
 Consensus quality: 183447 bases at least Q20  
 Estimated insert size: 186766; sum-of-contigs estimation  
 Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

----- NOTE: Estimated insert size may differ from sequence length  
 (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 5 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 25301: contig of 25301 bp in length  
 \* 25302 25401: gap of unknown length  
 \* 25402 48684: contig of 23263 bp in length  
 \* 48685 48764: gap of unknown length  
 \* 48765 93797: contig of 45033 bp in length  
 \* 93798 93897: gap of unknown length  
 \* 93898 135294: contig of 41397 bp in length  
 \* 135295 135395: gap of unknown length  
 \* 135396 186314: contig of 50920 bp in length.

FEATURES  
 Location/Qualifiers  
 1..186314  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="12"  
 /clone="RP11-709E21A"

ORIGIN  
 Query Match 91.1%; Score 16.4; DB 2; Length 186314;  
 Best Local Similarity 94.4%; Pred. No. 2.5e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGTTACTTGCTG 18  
 |||||  
 Db 178879 ATGCTTGTTACTTGCTG 178862

RESULT 36  
 AC122284/c

LOCUS  
 Mus musculus chromosome 6 clone RP23-246A5, WORKING DRAFT SEQUENCE,  
 6 unordered pieces.  
 AC122284  
 AC122284.4 GI:46879407  
 HTG; HTGS PHASE1; HTGS DRAFT; HTGS\_ACTIVEFIN.  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

ACCESSION  
 AC122284  
 VERSION  
 AC122284.4  
 GI:46879407  
 KEYWORDS  
 HTG; HTGS PHASE1; HTGS DRAFT; HTGS\_ACTIVEFIN.  
 SOURCE  
 Mus musculus  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 AUTHORS  
 Wilson, R.K.  
 TITLE  
 The sequence of Mus musculus clone  
 JOURNAL  
 Unpublished  
 REFERENCE  
 2 (bases 1 to 193985)  
 McPherson, J.D. and Waterston, R.H.  
 AUTHORS  
 McPherson, J.D. and Waterston, R.H.  
 TITLE  
 Direct Submission  
 JOURNAL  
 Submitted (23-MAY-2002) Genome Sequencing Center, 4444 Forest Park  
 Parkway, St. Louis, MO 63108, USA  
 3 (bases 1 to 193985)  
 REFERENCE  
 3 (bases 1 to 193985)  
 AUTHORS  
 Wilson, R.K.  
 TITLE  
 Direct Submission  
 JOURNAL  
 Submitted (30-APR-2004) Genome Sequencing Center, 4444 Forest Park  
 Parkway, St. Louis, MO 63108, USA  
 On Apr 30, 2004 this sequence version replaced gi:38229417.

COMMENT  
 ----- Genome Center -----  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: <http://genome.wustl.edu>  
 Contact: [submissions@watson.wustl.edu](mailto:submissions@watson.wustl.edu)  
 ----- Project Information -----  
 Center project name: M.BA0246A05  
 ----- Summary Statistics -----  
 Sequencing vector: M13; 0%  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 192391 bases at least Q40  
 Consensus quality: 192924 bases at least Q30  
 Consensus quality: 193306 bases at least Q20

\* NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

```

1 1173: contig of 1173 bp in length
1174 1273: gap of unknown length
1274 2330: contig of 1057 bp in length
2330 2431: gap of unknown length
2431 3593: contig of 1163 bp in length
3593 3694: gap of unknown length
3694 4999: contig of 1306 bp in length
4999 5099: gap of unknown length
5099 38451: contig of 33352 bp in length
38451 38551: gap of unknown length
38551 193985: contig of 155434 bp in length.

```

## FEATURES

## Source

```

1..193985
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="6"
/clone="RP23-246A5"

```

## misc\_feature

```

1..1173
/note="assembly_name:Contig18"

```

## misc\_feature

```

1274..2330
/note="assembly_name:Contig31"

```

## misc\_feature

```

2431..3593
/note="assembly_name:Contig42"

```

## misc\_feature

```

3694..4999
/note="assembly_name:Contig45"

```

## misc\_feature

```

5100..38451
/note="assembly_name:Contig49"

```

## misc\_feature

```

38552..193985
/note="assembly_name:Contig50"
clone_end:SP6
vector_side:left"

```

## ORIGIN

```

Query Match      91.1%; Score 16.4; DB 2; Length 193985;
Best Local Similarity 94.4%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 ATGCTTGTTACTTGCTG 18
|||||

```

```

Db 47924 ATGCTTGTTACTTGCTG 47907
|||||

```

## RESULT 37

## AC005674

```

LOCUS Homo sapiens chromosome 4 clone RP11-448G15, complete sequence.
DEFINITION AC005674.1 199450 bp DNA linear PRI 27-FEB-2001
ACCESSION AC005674
VERSION AC005674.11 GI:13129492
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 199450)
Submitted (11-SEP-1998) Department of Genetics, Stanford Human
Genome Center, 855 California Avenue, Palo Alto, CA 94304, USA
3 (bases 1 to 199450)
DOE Joint Genome Institute and Stanford Human Genome Center.

```

```

REFERENCE
AUTHORS Stone,N.E., Schmutz,J.J., Cox,D.R. and Myers,R.M.
TITLE Direct Submission
JOURNAL Unpublished

```

```

REFERENCE
AUTHORS Stone,N.E., Schmutz,J.J., Cox,D.R. and Myers,R.M.
TITLE Direct Submission
JOURNAL Unpublished

```

```

REFERENCE
AUTHORS Stone,N.E., Schmutz,J.J., Cox,D.R. and Myers,R.M.
TITLE Direct Submission
JOURNAL Unpublished

```

```

REFERENCE
AUTHORS Stone,N.E., Schmutz,J.J., Cox,D.R. and Myers,R.M.
TITLE Direct Submission
JOURNAL Unpublished

```

```

REFERENCE
AUTHORS Stone,N.E., Schmutz,J.J., Cox,D.R. and Myers,R.M.
TITLE Direct Submission
JOURNAL Unpublished

```

```

REFERENCE
AUTHORS Stone,N.E., Schmutz,J.J., Cox,D.R. and Myers,R.M.
TITLE Direct Submission
JOURNAL Unpublished

```

## TITLE

## JOURNAL

## COMMENT

Direct Submission  
Submitted (27-FEB-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
On Feb 27, 2001 this sequence version replaced gi:5757495.  
Finishing Completed at Stanford Human Genome Center  
www-shgc.stanford.edu  
Quality: Phrap Quality >=40 99.9% of Sequence;  
Estimated Total Number of Errors is 0.2.

## STS Content:

```

SHGC-51391 G34042
SHGC-69010 G41975
SHGC-50921 G33945
SHGC-25155 G31610
SHGC-51591 G34129
SHGC4-1311 G33196.

```

## FEATURES

## source

```

Location/Qualifiers
1..199450
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="4"
/clone="RP11-448G15"

```

## ORIGIN

```

Query Match      91.1%; Score 16.4; DB 9; Length 199450;
Best Local Similarity 94.4%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 ATGCTTGTTACTTGCTG 18
|||||

```

```

Db 104244 ATGCTTGTTACTTGCTG 104261
|||||

```

## RESULT 38

## AC117260/c

```

LOCUS Mus musculus BAC clone RP24-498G10 from chromosome 18, complete
sequence.
DEFINITION AC117260
VERSION AC117260.3 GI:23334842
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 211919)
Submitted (25-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Way, St. Louis, MO 63108, USA
2 (bases 1 to 211919)
Submitted (08-APR-2002) Genome Sequencing Center, 4444 Forest Park
Way, St. Louis, MO 63108, USA
4 (bases 1 to 211919)
Submitted (25-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Way, St. Louis, MO 63108, USA
5 (bases 1 to 211919)
Submitted (27-SEP-2002) Genome Sequencing Center, 4444 Forest Park
Way, St. Louis, MO 63108, USA
6 (bases 1 to 211919)
Submitted (13-NOV-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

```

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## AUTHORS

## TITLE

## JOURNAL

## AUTHORS

## TITLE

## JOURNAL

## AUTHORS

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## TITLE

## JOURNAL

## COMMENT

On Sep 27, 2002 this sequence version replaced gi:21206422.

----- Genome Center  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: <http://genome.wustl.edu>  
 Contact: [submissions@watson.wustl.edu](mailto:submissions@watson.wustl.edu)  
 ----- Summary Statistics  
 Center project name: M\_BB0498G10  
 -----

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

## MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

## SOURCE INFORMATION:

The RPCI-24 BAC library has been constructed by Pieter de Jong and coworkers (<http://www.chori.org>) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at <http://www.chori.org>

## NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone.

FEATURES  
source

1. 211919  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 /chromosome="18"  
 /map="18"  
 /clone="RP24-498G10"  
 /clone\_lib="RPCI-24"  
 1108..1170  
 /rpt\_family="CR1"  
 2516..2645  
 /rpt\_family="L1"  
 2772..2872  
 /rpt\_family="Alu"  
 3823..4147  
 /rpt\_family="MaLR"  
 6238..7257  
 /rpt\_family="L1"  
 7310..7645  
 /rpt\_family="MaLR"  
 7660..7723  
 /rpt\_family="ERV1"  
 7774..7989  
 /rpt\_family="L1"  
 8107..8270  
 /rpt\_family="L1"  
 8785..9015  
 /rpt\_family="MaLR"  
 10664..11013  
 /rpt\_family="MaLR"  
 13198..13495  
 /rpt\_family="L1"  
 14002..14067  
 /rpt\_family="ERV1"  
 16932..17011

repeat\_region  
 17320..17454  
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 17349..17501  
 /rpt\_family="Alu"  
 repeat\_region  
 17830..18177  
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 22931..23038  
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 25893..25994  
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 27545..27647  
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 28146..28264  
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 29898..30133  
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 30138..30202  
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 30576..30781  
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 33604..33669  
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 33701..33805  
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 33751..33826  
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 33836..34002  
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 35142..35220  
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 36186..36555  
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 36614..36962  
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 36996..37306  
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 37326..37806  
 /rpt\_family="L1"  
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 37823..38195  
 /rpt\_family="L1"  
 repeat\_region  
 40676..40857  
 /rpt\_family="L1"  
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 43626..44255  
 /rpt\_family="MIR"  
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 44690..44978  
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 45590..45775  
 /rpt\_family="B4"  
 repeat\_region  
 45843..45941  
 /rpt\_family="MER2\_type"  
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 46883..47043  
 /rpt\_family="L1"  
 repeat\_region  
 49416..49633  
 /rpt\_family="B4"  
 repeat\_region  
 49807..49922  
 /rpt\_family="B4"  
 repeat\_region  
 49979..50182  
 /rpt\_family="MER1\_type"  
 repeat\_region  
 50184..50238  
 /rpt\_family="MER1\_type"  
 repeat\_region  
 52622..52742  
 /rpt\_family="MIR"  
 repeat\_region  
 52936..53065  
 /rpt\_family="MER1\_type"  
 repeat\_region  
 53238..53581  
 /rpt\_family="ERVL"  
 repeat\_region  
 53600..53755  
 /rpt\_family="MaLR"  
 repeat\_region  
 53785..53926  
 /rpt\_family="MER1\_type"  
 repeat\_region  
 /rpt\_family="Alu"



repeat\_region 54554..54916  
/rpt\_family="MaLR"  
repeat\_region 55273..55665  
/rpt\_family="L1"  
repeat\_region 55867..55997  
/rpt\_family="L1"  
repeat\_region 56025..56566  
/rpt\_family="L1"  
repeat\_region 56559..56704  
/rpt\_family="L1"  
repeat\_region 59371..59430  
/rpt\_family="MERL\_type"  
repeat\_region 59830..60190  
/rpt\_family="MaLR"  
repeat\_region 60341..60447  
/rpt\_family="U6"

Query Match 91.18; Score 16.4; DB 10; Length 211919;  
Best Local Similarity 94.48; Pred No. 2.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 ATGCTTGCTACTGGCTG 18  
Db 161272 ATGCTTGCTACTGGCTG 161255  
|||||

RESULT 39  
AC110865/c  
LOCUS AC110865 220483 bp DNA linear HTG 19-NOV-2002  
DEFINITION Rattus norvegicus clone CH230-135020, WORKING DRAFT SEQUENCE.  
ACCESSION AC110865  
VERSION AC110865.5 GI:25072819  
KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT; HTGS\_FULLTOP.  
SOURCE Rattus norvegicus  
ORGANISM Rattus norvegicus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE 1 (bases 1 to 220483)  
Murny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,  
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,  
Anyalebechi,V., Ayoyagi,A., Ayodeji,M., Baca,E., Baden,H.,  
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,  
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Weinstock,G. and Gibbs,R.A.  
Direct Submission  
Unpublished  
2 (bases 1 to 220483)  
Worley,K.C.  
Direct Submission  
Submitted (16-FEB-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 220483)  
Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Nov 19, 2002 this sequence version replaced gi:23465753.  
The sequence in this assembly is a combination of BAC based reads  
and whole genome shotgun sequencing reads assembled using Atlas  
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described  
in the feature table below represents a scaffold in the Atlas  
assembly (a 'contig-scaffold'). Within each contig-scaffold,  
individual sequence contigs are ordered and oriented, and separated  
by sized gaps filled with Ns to the estimated size. The sequence  
may extend beyond the ends of the clone and there may be sequence  
contigs within a contig-scaffold that consist entirely of whole  
genome shotgun sequence reads. Both end sequences and whole genome  
shotgun sequence only contigs will be indicated in the feature  
table.  
----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GSQW  
Center clone name: CH230-195020  
----- Summary Statistics  
Assembly program: Phrap; version 0.990329  
Consensus quality: 199759 bases at least Q40  
Consensus quality: 202019 bases at least Q30  
Consensus quality: 203371 bases at least Q20  
Estimated insert size: 205444; sum-of-contigs estimation  
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation  
-----  
\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
consists of 1 contigs. Gaps between the contigs  
are represented as runs of N. The order of the pieces  
is believed to be correct as given, however the sizes  
of the gaps between them are based on estimates that have  
been provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1 220483: contig of 220483 bp in length.  
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FEATURES  
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## ORIGIN

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Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 204276 ATGGTGGTACTTGCTG 204259

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## RESULT 40

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LOCUS           Mus musculus BAC clone RP23-24B2 from chromosome 18, complete
DEFINITION      sequence.
ACCESSION       AC140455
VERSION         AC140455.2 GI:37951464
KEYWORDS        HTG.
SOURCE          Mus musculus (house mouse)
ORGANISM        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE       1 (bases 1 to 242533)
AUTHORS        Swearingen-Shahid,S., Shahid,S., Bielicki,L., Meyer,R. and
                Haakenson,W.
TITLE           The sequence of Mus musculus BAC clone RP23-24B2
JOURNAL         Unpublished (2001)
REFERENCE       2 (bases 1 to 242533)
AUTHORS        Wilson,R.
TITLE           Sequencing of Mus musculus
JOURNAL         Unpublished (2001)
REFERENCE       3 (bases 1 to 242533)
AUTHORS        McPherson,J.D. and Waterston,R.H.
TITLE           Direct Submission
JOURNAL         Submitted (23-FEB-2003) Genome Sequencing Center, 4444 Forest Park
                Parkway, St. Louis, MO 63108, USA
REFERENCE       4 (bases 1 to 242533)
AUTHORS        Wilson,R.K.
TITLE           Direct Submission
JOURNAL         Submitted (24-OCT-2003) Genome Sequencing Center, 4444 Forest Park
                Parkway, St. Louis, MO 63108, USA
REFERENCE       5 (bases 1 to 242533)
AUTHORS        Wilson,R.
TITLE           Direct Submission
JOURNAL         Submitted (25-NOV-2003) Department of Genetics, Washington
                University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT         On Oct 24, 2003 this sequence version replaced gi:28475726.
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Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu

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----- Summary Statistics
Center project name: M_BA0024B02
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

## MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

## SOURCE INFORMATION:

The RPCI-23 BAC Library has been constructed by Kazutoyo Oseigawa and Minako Tateno in the laboratory of Pieter de Jong (<http://www.chori.org>) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

## NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone. This clone is overlapped by AC117260 and AC131736.

## FEATURES

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Query Match          91.1%; Score 16.4; DB 10; Length 242533;
Best Local Similarity 94.4%; Pred. No. 2.4e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 1;

QY    1 ATGCTTGACTTGGCGTG 18
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RESULT 41
AC107416          244291 bp DNA linear HTG 11-OCT-2002
LOCUS            Rattus norvegicus clone CH230-208A8, WORKING DRAFT SEQUENCE.
DEFINITION       Rattus norvegicus clone CH230-208A8, WORKING DRAFT SEQUENCE.
ACCESSION        AC107416
VERSION          AC107416.4 GI:23793295
KEYWORDS         HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE           Rattus norvegicus (Norway rat)
ORGANISM         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                  Rattus.

REFERENCE
1 (bases 1 to 24291)
AUTHORS
Muzny,D.,Marie,, Metzker,M.,Lee,, Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Aisbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Ayodeji,M., Baca,E., Baden,H.,
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repeat_region      19215..19226 /rpt_family="L1"
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repeat_region      19227..19597 /rpt_family="MaLR"
                    67921..68263 /rpt_family="L1"
repeat_region      19598..20106 /rpt_family="L1"
                    68290..68392 /rpt_family="L1"
repeat_region      20123..20770 /rpt_family="L1"
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                    68568..68672 /rpt_family="ERVK"
repeat_region      24528..24721 /rpt_family="MaLR"
                    68985..69131 repeat_region
                    69131
Query Match          91.1%; Score 16.4; DB 10; Length 242533;
Best Local Similarity 94.4%; Pred. No. 2.4e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 1;
QY    1 ATGCTTGGTACTTGCGTG 18
Db     87826 ATGCTTGATCTTGCGTG 87809

RESULT 41
AC107416              244291 bp DNA linear HTG 11-OCT-2002
LOCUS               Rattus norvegicus clone CH230-208A8, WORKING DRAFT SEQUENCE.
DEFINITION           Rattus norvegicus clone CH230-208A8, WORKING DRAFT SEQUENCE.
ACCESSION            AC107416
VERSION              AC107416.4 GI:23793295
KEYWORDS              HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE                Rattus norvegicus (Norway rat)
ORGANISM              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                      Rattus.
REFERENCE             1 (bases 1 to 244291)
AUTHORS              Muzny,D.,Marrie,, Metzker,M.,Lee,, Abramson,S., Adams,C., Alder,J.,
                      Allen,C., Allen,H., Aisbrooks,S., Amin,A., Anguiano,D.,
                      Anyalebechi,V., Ayoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
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```

Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

# TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

Unpublished  
2 (bases 1 to 244291)  
Worley, K.C.

Direct Submission

Submitted (20-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 244291)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (11-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Oct 11, 2002 this sequence version replaced gi:21737494.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GPGB

Center clone name: CH230-208A8

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 213567 bases at least Q40

Consensus quality: 216388 bases at least Q30

Consensus quality: 217940 bases at least Q20

Estimated insert size: 217940 bases at least Q20

Quality coverage: 7X in Q20 bases; sum-of-contigs estimation

-----  
\* NOTE: Estimated insert size may differ from sequence length (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

\* This sequence will be replaced

\* by the finished sequence as soon as it is available and

\* the accession number will be preserved.

\* the accession number will be preserved.

\* the accession number will be preserved.

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\* the accession number will be preserved.

\* the accession number will be preserved.

\* the accession number will be preserved.

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clone\_end:Sp6"  
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/note="clone boundary"  
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site:EcoRI  
end\_sequence:RWBKN04TVB"  
234819..235718  
/note="clone boundary"  
clone\_end:T7  
site:EcoRI  
end\_sequence:RWBKN04TVB"  
241756..244291  
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clone\_end:T7"

ORIGIN

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Best Local Similarity 94.4%; Pred. No. 2.4e-02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGCTTGGCTG 18

DB 196445 ATGCTTGCTTGGCTG 196462

RESULT 42

AC118528

LOCUS

DEFINITION

AC118528.4 GI:25009710

HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ENRICHED.

SOURCE

Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 252813)

REFERENCE

AUTHORS

Muzny, D., Marie, Metzker, M., Lee, Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Center, A., Chacko, J., Chavez, D., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guavara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, J., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hires, S., Hladun, S.L., Hodgson, A., Hughes, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensu, L., Loulsegheh, H., Lozada, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,

Nwaokemele, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plummer, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajda, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soza, J., Steidle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, I., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlezyk, R., Woodson, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, P., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission  
Unpublished  
2 (bases 1 to 252813)  
Worley, K.C.

Direct Submission  
Submitted (18-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 252813)

Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Nov 15, 2002 this sequence version replaced gi:23267375.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GUTV  
Center clone name: CH230-159B3  
----- Summary Statistics  
Assembly program: Phrap; version 0.990329  
Consensus quality: 233732 bases at least Q40  
Consensus quality: 236563 bases at least Q30  
Consensus quality: 238332 bases at least Q20  
Estimated insert size: 244276; sum-of-contigs estimation  
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation  
-----  
\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.  
\* 1 243357: contig of 243357 bp in length  
\* 243358 243457: gap of unknown length

\* 243458 249505: contig of 6048 bp in length  
\* 249506 249605: gap of unknown length  
\* 249606 252813: contig of 3208 bp in length.

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/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-159B3"  
1. 1535  
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clone\_end:Sp6  
site:  
end\_sequence:BH315097"  
238009..238435  
/note="clone\_boundary"  
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site:  
end\_sequence:BH315095"  
241380..243357  
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clone\_end:T7"  
247865..249505  
/note="wgs\_end\_extension"  
clone\_end:T7"  
249605..250769  
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clone\_end:T7"

ORIGIN  
Query Match 91.1%; Score 16.4; DB 2; Length 252813;  
Best Local Similarity 94.4%; Pred. No. 2.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGGTACTTGCTG 18  
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Db 44287 ATGCTTGGTCTTGCTG 44304

RESULT 43  
AC098502/c  
LOCUS  
DEFINITION  
Rattus norvegicus clone CH230-38D10, \*\*\* SEQUENCING IN PROGRESS  
\*\*\*, 2 unordered pieces.  
AC098502  
VERSION  
AC098502.8 GI:30521825  
HTG; HTGS PHASE1; HTGS\_DRAFT; HTGS\_ENRICHED.  
KEYWORDS  
Rattus norvegicus  
SOURCE  
ORGANISM  
Rattus.  
REFERENCE  
1 (bases 1 to 262126)  
Muzny, D., Maric, M., Metzker, M., Lee, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Muzny, D., Maric, M., Metzker, M., Lee, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,

Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregiorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, S., Jiang, H., Johnson, B., Johnson, R., Joliver, A., Karpaty, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensheva, L., Loulseghe, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwackelme, O., Okwou, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzo, M., Quiroz, J., Rachin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Staimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, F., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, X., Zhou, X., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G., and Gibbs, R.A.

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Submitted (24-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 262126)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 10, 2003 this sequence version replaced gi:24955127.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Web site: BCM  
Web code: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
----- Project Information  
Center project name: GHFF  
Center clone name: CH230-38D10  
----- Summary Statistics  
Assembly program: Atlas 3.0;  
Consensus quality: 225037 bases at least Q40

Consensus quality: 227860 bases at least Q30  
Consensus quality: 229607 bases at least Q20  
Estimated insert size: 235266; sum-of-contigs estimation  
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation  
-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 2 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 260921: contig of 260921 bp in length  
\* 260922 261021: gap of unknown length  
\* 261022 262126: contig of 1105 bp in length.  
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misc\_feature  
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/note="wgs end extension  
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misc\_feature  
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end\_sequence:BH308749"  
misc\_feature  
complement(258115..258539)  
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site:EcoRI  
end\_sequence:BH308748"  
ORIGIN  
Query Match 91.1%; Score 16.4; DB 2; Length 262126;  
Best Local Similarity 94.4%; Pred. NO. 2.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGCTTGGTACTTGGCTG 18  
Db 95522 ATGCTTGGTACTTGGCTG 95505  
RESULT 44  
AC120474  
LOCUS  
DEFINITION  
Rattus norvegicus clone CH230-459E14, WORKING DRAFT SEQUENCE, 7  
unordered pieces.  
AC120474  
AC120474.4 GI:25008182  
HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.  
Rattus norvegicus (Norway rat)  
SOURCE  
Rattus norvegicus  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE  
1 (bases 1 to 262126)  
Muzny, D.M., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,  
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,  
Anyalebechi, V., Ayvagi, A., Ayodeji, M., Baca, E., Baden, H.,  
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,  
Biswas, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,  
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,  
Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Center, A.,  
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,

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Direct Submission  
Unpublished  
2 (bases 1 to 285212)  
Worley, K.C.

Direct Submission  
Submitted (07-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 285212)  
Rat Genome Sequencing Consortium.

Direct Submission  
Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Nov 15, 2002 this sequence version replaced gi:23907737.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu

----- Project Information  
Center project name: GXHL  
Center clone name: CH230-459E14  
----- Summary Statistics  
Assembly program: Phrap; version 0.990329  
Consensus quality: 18533 bases at least Q40  
Consensus quality: 18748 bases at least Q30  
Consensus quality: 188612 bases at least Q20  
Estimated insert size: 186762; sum-of-contigs estimation  
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation  
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\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 7 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
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ACCESSION  
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REFERENCE AUTHORS	1 (bases 1 to 314957) Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galle,R.F., George,R.A., Lewis,S.E., Richards,S., Ashburner,M., Henderson,S.N., Sutton,G.G., Wortman,J.R., Yandell,M.D., Zhang,Q., Chen,L.X., Brannon,R.C., Rogers,Y.H., Blazej,R.G., Champe,M., Pfeiffer,B.D., Wan,K.H., Doyle,C., Baxter,E.G., Helt,G., Nelson,C.R., Gabor,G.L., Abail,J.F., Agbayani,A., An,H.J., Andrews-Pfannkoch,C., Baldwin,D., Ballew,R.M., Basu,A., Baxendale,J., Bayraktaroglu,L., Beasley,B.M., Beeson,K.Y., Benos,P.V., Berman,B.P., Bhandari,D., Bolshakov,S., Borkova,D., Botchan,M.R., Bouck,J., Brockstein,P., Brothier,P., Burris,K.C., Busam,D.A., Butler,H., Cadieu,E., Center,A., Chandra,I., Cherry,J.M., Cawley,S., Dahlke,C., Davenport,L.B., Davies,P., de Pablos,B., Delcher,A., Deng,Z., Mays,A.D., Dew,I., Dietz,S.M., Dodson,K., Doup,L.E., Downes,M., Dugan-Rocha,S., Dunkov,B.C., Dunn,P., Durbin,K.J., Evangelista,C.C., Ferraz,C., Ferriera,S., Fleischmann,W., Fosler,C., Gabrielson,A.E., Garg,N.S., Gelbart,W.M., Glasser,K., Glodde,A., Gong,F., Gorrell,J.H., Gu,Z., Guan,P., Harris,M., Harris,N.L., Harvey,D., Heiman,T.J., Hernandez,J.R., Houck,J., Hostin,D., Houston,K.A., Howland,T.J., Wei,M.H., Iqbal,M., Jaiswal,M., Kalish,B., Karp,G.H., Ke,Z., Kernison,J.A., Ketchum,K.A., Kimmel,B.E., Kodira,C.D., Kraft,C., Kravitz,S., Kulp,D., Lai,Z., Lasko,P., Lei,Y., Levitsky,A.A., Li,J., Li,Z., Liang,Y., Lin,X., Liu,X., Mattei,B., McIntosh,T.C., McLeod,M.P., McPherson,D., Merkulov,G., Milshina,N.V., Mobarry,C., Morris,J., Moshrefi,A., Mount,S.M., Moy,M., Murphy,B., Murphy,L., Muzny,D.M., Nelson,D.L., Nelson,D.R., Nelson,K.A., Nixon,K., Nuskern,D.R., Pacleb,J.M., Palazzolo,M., Pittman,G.S., Pan,S., Pollard,J., Puri,V., Reese,M.G., Reinert,K., Remington,K., Saunders,R.D., Scheeler,F., Shen,H., Shue,B.C., Siden-Kiamis,I., Simpson,M., Skupski,M.P., Smith,T., Spier,E., Spradling,A.C., Stapleton,M., Strong,R., Sun,B., Svirskas,R., Tector,C., Turner,R., Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wasserman,D.A., Weinstock,G.M., Weissbach,J., Williams,S.M., Woodage,T., Worley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Ye,R.F., Zaveri,J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X.H., Zhong,F.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O., Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.
TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	The genome sequence of <i>Drosophila melanogaster</i> Science 287 (5461), 2185-2195 (2000) 20196006 10731132 2 (bases 1 to 314957) Celniker,S.E., Wheeler,D.A., Kronmiller,B., Carlson,J.W., Halpern,A., Patel,S., Adams,M., Champe,M., Dugan,S.P., Frise,E., Hedgson,A., George,R.A., Hoskins,R.A., Laverdy,T., Muzny,D.M., Nelson,C.R., Pacleb,J.M., Park,S., Pfeiffer,B.D., Richards,S., Sodergren,E.J., Svirskas,R., Tabor,P.E., Wan,K., Stapleton,M., Sutton,G.G., Venter,J.C., Weinstock,G., Scherer,S.E., Myers,E.W., Gibbs,R.A. and Rubin,G.M. Finishing a whole-genome shotgun: release 3 of the <i>Drosophila</i> melanogaster euchromatic genome sequence Genome Biol. 3 (12), RESEARCH0079 (2002) 2426065 12537568
TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	3 (bases 1 to 314957) Mitra,S., Crosby,M.A., Murgall,C.J., Matthews,B.B., Campbell,K.S., Hradecky,P., Huang,Y., Kaminker,J.S., Willburn,G.H., Prochnik,S.E., Smith,C.D., Tupy,J.L., Whitfield,E.J., Bayraktaroglu,L., Berman,B.P., Bettencourt,B.R., Celniker,S.E., de Grey,A.D., Drysdale,R.A., Harris,N.L., Richter,J., Russo,S., Schroeder,A.J., Shu,S.Q., Stapleton,M., Yamada,C., Ashburner,M., Gelbart,W.M., Rubin,G.M. and Lewis,S.E. Annotation of the <i>Drosophila melanogaster</i> euchromatic genome: a systematic review Genome Biol. 3 (12), RESEARCH0083 (2002)
TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	4 (bases 1 to 314957) Kaminker,J.S., Bergman,C.M., Kronmiller,B., Carlson,J., Svirskas,R., Patel,S., Frise,E., Wheeler,D.A., Lewis,S.E., Rubin,G.M., Ashburner,M. and Celniker,S.E. The transposable elements of the <i>Drosophila melanogaster</i> euchromatin: a genomics perspective Genome Biol. 3 (12), RESEARCH0084 (2002) 22426067 12537573 5 (bases 1 to 314957) Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J. Direct Submission Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA 6 (bases 1 to 314957) FlyBase Direct Submission Submitted (06-SEP-2002) University of California Berkeley, 539 Life Sciences Addition, Berkeley, CA 94720, USA 7 (bases 1 to 314957) FlyBase Direct Submission Submitted (10-MAR-2004) FlyBase, Harvard University, Biological Laboratories, 16 Divinity Avenue, Cambridge, MA 02138, USA On Sep 16, 2002 this sequence version replaced gi:10727365. Location/Qualifiers 1. 314957 /organism="Drosophila melanogaster" /mol_type="genomic DNA" /db_xref="taxon:7227" /chromosome="2L" complement(5211..8075) /locus_tag="CG3119" /map="23B3-23B3" /db_xref="FLYBASE:FBgn0031466" complement(join(<5211..5444,5499..5795,7437..7530, 7590..8075)) /locus_tag="CG3119" /product="CG3119-PA" /db_xref="FLYBASE:FBgn0031466" complement(join(5211..5444,5499..5795,7437..7530, 7590..8032)) /locus_tag="CG3119" /codon_start=1 /product="CG3119-PA" /protein_id="AAF51199.2" /db_xref="GI:4544959" /translation="MTAKMLRSQHLTLGTGMAGFVLAFVLLLYVYDVSRTPCWSST STMTATARIEDGPPRIICMLVLTCPENVSLARSVYETWGORCSRLIFASSEDYEP LGVVVVEPTGGYGVYKSVYNSVMSGASVILSREALHFAQYAESVLCQPKMGIE DPYNGICMQVGVHFVNSTHALDGDTPKEMPLENYSANDNTTIPENURLMSLRV ETGLACSNYSVAFYASRERMFYELIYHLVDENQISERGHRSRLTSLTRRP PLEDNSIKOLLQMSKPDNF" complement(join(6343..6422,7437..7530,7590..8075)) /locus_tag="CG3119" /product="CG3119-RB" /db_xref="FLYBASE:FBgn0031466" complement(join(6405..6422,7437..7530,7590..8032)) /locus_tag="CG3119" /codon_start=1 /product="CG3119-PB" /protein_id="AANI10390.1" /db_xref="GI:22945330" /db_xref="FLYBASE:FBgn0031466" /translation="MTAKMLRSQHLTLGTGMAGFVLAFVLLLYVYDVSRTPCWSST STMTATARIEDGPPRIICMLVLTCPENVSLARSVYETWGORCSRLIFASSEDYEP LGVVVVEPTGGYGVYKSVYNSVMSGASVILSREALHFAQYAESVLCQPKMGIE DPYNGICMQVGVHFVNSTHALDGDTPKEMPLENYSANDNTTIPENURLMSLRV ETGLACSNYSVAFYASRERMFYELIYHLVDENQISERGHRSRLTSLTRRP PLEDNSIKOLLQMSKPDNF"



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Duchaud, E., Rusniok, C., Frangeul, L., Buchrieser, C., Taurit, S.,  
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 Dezeille, S., Freyssinet, G., Gaudriault, S., Givaudan, A., Glaser, P.,  
 Medigue, C., Lanols, A., Powell, K., Sigulier, P., Wingate, V.,  
 Zouine, M., Boemare, N., Danchin, A. and Kunst, F.  
 Complete genome sequence of the entomopathogenic bacterium  
 Photobacterium luminescens  
 Nat. Biotechnol. 11 (1) (2003) In press

Duchaud, E., Frangeul, L., Rusniok, C. and Kunst, F.  
 Direct Submission  
 Submitted (23-APR-2003) L. Frangeul, Institut Pasteur, Genopole, 25  
 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail:  
 lfrangeul@pasteur.fr, fkunst@pasteur.fr

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 TATQSYPDHSCIRHLEFQAKKSPDATALVYEQILSYANLANCANLAHQILALGV  
 TPDQVAVCVSRSPANVAGLAVLKAGAYVPLDPAPSAHLAHTLTPAARLVIALDK  
 AKGVALGREALTGLVLDNIPNOVDNPOISGLTSLHAYVITSSTGTPGKGVMI  
 EHKNTVNYLYAQAQAFETEEIREVLFSTSMNFDLSIFCFVLSQCATIHLVEDALS  
 MCHALPVLINSVPSAMKELLQALMASVHTNVLNAGELKCALTEQIETQICORLC  
 NLYGSETTYRNLPIQKGRDIIESIRPNTIRLYLLDENGQVPLGVGVEIYIGG  
 AGVARGYFNRPDLTFRFLIDPFDVDFARMTRTGLDARYFDGLENLEFLGRNDQVKI  
 RGFRIFEPGIEEARLMEHPAVSEAVILALDDQDKRLVAVVAEAEVLNIRUHLAHS  
 VLPDYVMVPAFVCLDAFPLTPNGKLDRLRALPGEEDFARQIYAAPSGEMETTLAAIV



```
source
1. 349980
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/db_xref="taxon:29488"
/notes="sequence length too big (460203). Split into 2
sequences. -seq 00036: 1 to 349980-seq 10785: 300001 to
460203"

ORIGIN
Query Match 91.1%; Score 16.4; DB 6; Length 349980;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGGTACTTGGCTG 18
Db 193035 ATGCTTGGTATTGGCTG 193052

RESULT 48
AC021602/c
LOCUS 105866 bp DNA linear HTG 14-MAY-2000
DEFINITION Homo sapiens clone RP11-214H18, WORKING DRAFT SEQUENCE, 26
unordered pieces.
ACCESSION AC021602
VERSION AC021602.2 GI:7801430
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 105866)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Boguslavskiy,I., Bouckhalter,B., Brown,A., Burkett,G., Castle,A.,
Choepel,Y., Collangelo,M., Collins,S., Collymore,A., Cooke,P.,
DeArellano,K., Dewar,K., Domino,M., Doyle,M., Fenesfor,J.,
Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Headford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Iehoczky,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheeters,R., Meldrim,J., Merens,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Rhmann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 14, 2000 this sequence version replaced gi:6705497.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L5805
Center clone name: 214.H.18
----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 93332 bases at least Q40
Consensus quality: 99518 bases at least Q30

Consensus quality: 101729 bases at least Q20
Insert size: 74000; agarose-fp
Insert size: 10366; sum-of-contigs
Quality coverage: 11.1 in Q20 bases; agarose-fp
Quality coverage: 7.9 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 26 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1376: contig of 1376 bp in length
* 1377 gap of 100 bp
* 1477 contig of 1174 bp in length
* 2651 gap of 100 bp
* 2751 contig of 1132 bp in length
* 3883 gap of 100 bp
* 3983 contig of 1060 bp in length
* 5043 gap of 100 bp
* 5142 contig of 1108 bp in length
* 6251 gap of 100 bp
* 6351 contig of 1106 bp in length
* 7457 gap of 100 bp
* 7557 contig of 1610 bp in length
* 9167 gap of 100 bp
* 9266 contig of 1777 bp in length
* 1043 gap of 100 bp
* 1143 contig of 1022 bp in length
* 1144 gap of 100 bp
* 12166 contig of 1279 bp in length
* 12666 gap of 100 bp
* 13545 gap of 100 bp
* 13645 contig of 1727 bp in length
* 1372 gap of 100 bp
* 1472 contig of 1331 bp in length
* 16803 gap of 100 bp
* 16903 contig of 1608 bp in length
* 18510 gap of 100 bp
* 18511 contig of 1417 bp in length
* 20027 gap of 100 bp
* 20127 contig of 1870 bp in length
* 20228 gap of 100 bp
* 21797 contig of 2303 bp in length
* 21798 gap of 100 bp
* 21898 contig of 100 bp
* 24201 gap of 100 bp
* 24300 contig of 1777 bp in length
* 26078 gap of 100 bp
* 26177 contig of 1385 bp in length
* 27562 gap of 100 bp
* 27663 contig of 1834 bp in length
* 29496 gap of 100 bp
* 29596 contig of 3863 bp in length
* 33459 gap of 100 bp
* 33559 contig of 4102 bp in length
* 37661 gap of 100 bp
* 37662 contig of 2975 bp in length
* 40737 gap of 100 bp
* 40837 contig of 3617 bp in length
* 44553 gap of 100 bp
* 44554 contig of 4990 bp in length
* 49544 gap of 100 bp
* 49544 contig of 28265 bp in length
* 77908 gap of 100 bp
* 78008 contig of 100 bp
* 78009 contig of 27858 bp in length.
* 78009 105866: contig of 27858 bp in length.
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* Location/Qualifiers
* 1..105866
* /organism="Homo sapiens"
* /mol_type="genomic DNA"
* /db_xref="taxon:9606"
* /clone_lib="RP11-214H18"
* /clone_lib="RPC1-11 Human Male BAC"
* 1..1376
* misc_feature
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misc_feature /note="assembly_fragment"
1477..2650
misc_feature /note="assembly_fragment"
2751..3882
misc_feature /note="assembly_fragment"
3983..5042
misc_feature /note="assembly_fragment"
5143..6250
misc_feature /note="assembly_fragment"
6351..7456
misc_feature /note="assembly_fragment"
7557..9166
misc_feature /note="assembly_fragment"
9267..11043
misc_feature /note="assembly_fragment"
11144..12165
misc_feature /note="assembly_fragment"
12266..13544
misc_feature /note="assembly_fragment"
13645..15371
misc_feature /note="assembly_fragment"
15472..16802
misc_feature /note="assembly_fragment"
16903..18510
misc_feature /note="assembly_fragment"
18611..20027
misc_feature /note="assembly_fragment"
20128..21797
misc_feature /note="assembly_fragment"
21898..24200
misc_feature /note="assembly_fragment"
24301..26077
misc_feature /note="assembly_fragment"
26178..27562
misc_feature /note="assembly_fragment"
27663..29496
misc_feature /note="assembly_fragment"
clone_end:T7
vector_side:right
vector_start:33459
misc_feature /note="assembly_fragment"
33560..37661
misc_feature /note="assembly_fragment"
37762..40736
misc_feature /note="assembly_fragment"
clone_end:SP6
vector_side:left
vector_start:44453
misc_feature /note="assembly_fragment"
44554..49543
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49644..77508
misc_feature /note="assembly_fragment"
78009..105866
misc_feature /note="assembly_fragment"

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## ORIGIN

Query Match 88.9%; Score 16; DB 2; Length 105866;  
 Best Local Similarity 100.0%; Pred. NO. 4.4e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTTGCTACTTGGC 16  
 |||||

Db 91742 ATGCTTGCTACTTGGC 91727

## RESULT 49

HS212P9  
 LOCUS HS212P9 148540 bp DNA linear PRI 05-JUN-2003  
 DEFINITION Human DNA sequence from clone Rpl-212P9 on chromosome 1p34.1-35,  
 complete sequence.  
 ACCESSION AL009181  
 VERSION AL009181.1 GI:2853179

## KEYWORDS

HTG.  
 Homo sapiens (human)

## SOURCE

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 148540)

## AUTHORS

Grafham,D.

## TITLE

Direct Submission

## JOURNAL

Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

## COMMENT

On Feb 9, 1998 this sequence version replaced gi:2655915.  
 ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: humquery@sanger.ac.uk  
 -----

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at  
 http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at  
 http://www.sanger.ac.uk/HGP/Chr1

Rpl-212P9 is from the library RPl-1 constructed by the group of Pieter de Jong. For further details see  
 http://www.chori.org/bacpac/home.htm

## VECTOR: pCYPAC2

IMPORTANT: This sequence is not the entire insert of clone RPl-212P9. It may be shorter because we sequence overlapping sections only once, except for a short overlap.

## FEATURES

Location/Qualifiers  
 1..148540

/organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="RZPD:RPl-212P9" /db\_xref="taxon:9606"  
 /chromosome="1"  
 /map="p34.1-35"  
 /clone="RPl-212P9"  
 /clone\_lib="RPl-1"

complement(1..61)  
 /note="Alu repeat: matches 2..62 of consensus"  
 complement(135..365)  
 /note="Alu repeat: matches 61..292 of consensus"  
 465..476  
 /note="3.0 copies 4 mer TAAA 24% conserved"  
 481..603  
 /note="FLAM\_C repeat: matches 5..126 of consensus"  
 610..628  
 /note="3.8 copies 5 mer TAAAT 38% conserved"  
 892..1178  
 /note="Alu repeat: matches 5..291 of consensus"  
 1218..1230  
 /note="2.6 copies 5 mer TTTC 26% conserved"  
 1498..1838

repeat\_region

repeat\_region

repeat\_region

repeat\_region

repeat\_region

repeat\_region

misc\_feature

repeat\_region /note="match: STS: Em:AL009314"  
1704. .1883  
/note="L2 repeat: matches 3120. .3307 of consensus"  
1922. .2003  
/note="2.4 copies 5 mer TATAA 24% conserved"  
2094. .2107  
/note="2.3 copies 6 mer TGTTC 28% conserved"  
2244. .2256  
/note="6.5 copies 2 mer TC 26% conserved"  
2256. .2275  
/note="2.2 copies 9 mer TTGCCTTG 40% conserved"  
2949. .3235  
/note="AluSc repeat: matches 1. .303 of consensus"  
4236. .4245  
/note="2.5 copies 4 mer AGCA 20% conserved"  
4409. .4422  
/note="2.0 copies 7 mer AATGAAT 28% conserved"  
4470. .4588  
/note="MER5B repeat: matches 1. .154 of consensus"  
4610. .4787  
/note="MER5A repeat: matches 2. .185 of consensus"  
4976. .4995  
/note="5.0 copies 4 mer GCAT 31% conserved"  
4993. .5010  
/note="4.5 copies 4 mer CATT 27% conserved"  
complement(5011. .5065)  
/note="AluJ/FRAM repeat: matches 228. .282 of consensus"  
5260. .5563  
/note="L1MC5 repeat: matches 7347. .7636 of consensus"  
5564. .5727  
/note="AluSg repeat: matches 1. .167 of consensus"  
5985. .5996  
/note="2.0 copies 6 mer TTCCC 24% conserved"  
6049. .6058  
/note="3.3 copies 3 mer ATT 20% conserved"  
complement(6060. .6346)  
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6373. .6386  
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6415. .6425  
/note="2.2 copies 5 mer ATTTT 22% conserved"  
complement(6691. .7020)  
/note="AluJb repeat: matches 1. .304 of consensus"  
complement(6950. .7348)  
misc\_feature /note="match: STS: Em:251524"  
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7265. .7274  
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7458. .7750  
/note="AluSg repeat: matches 1. .294 of consensus"  
7939. .7949  
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8092. .8101  
/note="2.5 copies 4 mer ATAC 20% conserved"  
8220. .8330  
/note="MIR repeat: matches 21. .136 of consensus"  
8355. .8366  
/note="2.4 copies 5 mer ATTAA 24% conserved"  
8374. .8690  
/note="L1ME3B repeat: matches 5587. .5930 of consensus"  
8691. .8997  
/note="AluSg repeat: matches 1. .307 of consensus"  
8998. .9144  
/note="L1ME3B repeat: matches 5930. .5978 of consensus"  
complement(9145. .9430)  
/note="AluJb repeat: matches 1. .290 of consensus"  
9431. .9629  
/note="L1ME3B repeat: matches 5978. .6193 of consensus"  
complement(9633. .9924)  
/note="AluSg repeat: matches 1. .290 of consensus"  
complement(10057. .10360)  
/note="AluYd2 repeat: matches 1. .299 of consensus"

repeat\_region 10603. .10612  
/note="10.0 copies 1 mer A 20% conserved"  
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/note="AluSx repeat: matches 1. .292 of consensus"  
11142. .11158  
/note="4.2 copies 4 mer GTTT 34% conserved"  
complement(11159. .11456)  
/note="AluSc repeat: matches 1. .306 of consensus"  
11699. .11712  
/note="2.0 copies 7 mer AAAACAT 28% conserved"  
11924. .11935  
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12053. .12067  
/note="2.1 copies 7 mer TAAATA 30% conserved"  
12186. .12294  
/note="AluY repeat: matches 1. .109 of consensus"  
12307. .12393  
/note="AluSg/x repeat: matches 211. .297 of consensus"  
12437. .12446  
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12536. .12548  
/note="3.2 copies 4 mer ATTC 26% conserved"  
13003. .13014  
/note="3.0 copies 4 mer CCTT 24% conserved"  
complement(13481. .13767)  
/note="AluJb repeat: matches 19. .308 of consensus"  
13775. .14057  
/note="AluSx repeat: matches 18. .305 of consensus"  
complement(14078. .14920)  
/note="L1M1 repeat: matches 5442. .6301 of consensus"  
complement(14921. .15221)  
/note="AluSx repeat: matches 1. .305 of consensus"  
complement(15222. .15369)  
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15372. .15381  
/note="2.5 copies 4 mer TTCC 20% conserved"  
15646. .16492  
/note="MER21B repeat: matches 1. .857 of consensus"  
16524. .16628  
/note="L1ME4 repeat: matches 5965. .6087 of consensus"  
complement(16670. .16978)  
/note="AluSp repeat: matches 1. .311 of consensus"  
complement(17200. .17496)  
/note="AluJb repeat: matches 1. .295 of consensus"  
complement(17926. .18221)  
/note="AluSx repeat: matches 2. .297 of consensus"  
18555. .18787  
/note="MTRH1 repeat: matches 327. .550 of consensus"  
18850. .19154  
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Best Local Similarity 100.0%; Pred.No. 4.2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGCTTGTTGCTTGGC 16  
|||||  
Db 64076 ATGCTTGTTGCTTGGC 64091  
RESULT 50  
AL335064/c 157256 bp DNA linear VRT 16-APR-2003  
LOCUS Zebrafish DNA sequence from clone CH211-153K23, complete sequence.  
DEFINITION AL335064  
ACCESSION AL335064  
VERSION AL335064.7 GI:29498207  
KEYWORDS HTG.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
REFERENCE 1 (bases 1 to 157256)  
AUTHORS Wood,J.

TITLE  
JOURNAL

Direct Submission  
Submitted (16-APR-2003) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
On Apr 2, 2003 this sequence version replaced gi:29125198.

## COMMENT

----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: zfish-help@sanger.ac.uk  
-----

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhiron Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see [http://www/Projects/D\\_rerio/fishmask.shtml](http://www/Projects/D_rerio/fishmask.shtml) CH211-153K23 is from a CHORI-211 BAC library  
VECTOR: PTARBAC2.1.

## FEATURES

## source

1. 157256  
Location/Qualifiers  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="CH211-153K23"  
/clone\_lib="CHORI-211"

## ORIGIN

Query Match 88.9%; Score 16; DB 5; Length 157256;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTTGCTACTGGC 16

|||||

D5 133841 ATGCTTGCTACTGGC 133826

Search completed: December 3, 2004, 03:10:02  
Job time : 634.921 secs

GenCore version 5.1.6		Copyright (c) 1993 - 2004 CompuGen Ltd.	
OM nucleic - nucleic search, using sw model			
Run on:	December 3, 2004, 02:05:35 ; Search time 1761.58 seconds (without alignments) 62.385 Million cell updates/sec		
Title:	US-10-050-189A-8		
Perfect score:	20		
Sequence:	1 gcagtttaattggagagtggt 20		
Scoring table: IDENTITY NUC			
Gapop 10.0 , Gapext 1.0			
Searched:	3694831 seqs, 2747406616 residues		
Total number of hits satisfying chosen parameters: 7389662			
Minimum DB seq length: 0			
Maximum DB seq length: 2000000000			
Post-processing: Minimum Match 0%			
Maximum Match 100%			
Listing first 1000 summaries			
Database : Published Applications NA:			
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:			
2: /cgn2_6/ptodata/2/pubpna/PTC_NEW_PUB.seq:			
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:			
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:			
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:			
6: /cgn2_6/ptodata/2/pubpna/PTCUS_PUBCOMB.seq:			
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:			
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:			
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:			
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:			
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:			
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:			
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:			
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:			
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:			
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:			
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:			
18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:			
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:			
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:			
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:			
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES			
Result No.	Query Match Length DB ID Description		
1	20 100.0 20 13 US-10-050-189A-8 Sequence 8, Appli		
2	20 100.0 66479 13 US-10-041-856-1 Sequence 1, Appli		
3	17 85.0 2298 17 US-10-437-963-65936 Sequence 65936, A		
4	16.8 84.0 565 13 US-10-027-632-275091 Sequence 275091, Sequence 275091,		
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C 41	15.8 79.0 2369 9 US-09-908-605B-20 Sequence 20, Appli		
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C 48	15.8 79.0 116858 13 US-10-087-192-547 Sequence 547, App		
49	15.8 79.0 135579 15 US-10-085-117-283 Sequence 283, App		
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C 53	15.4 77.0 464 9 US-09-864-761-17793 Sequence 11793, A		
C 54	15.4 77.0 464 9 US-09-864-761-6844 Sequence 6844, Ap		
C 55	15.4 77.0 589 13 US-10-027-632-89997 Sequence 89997, A		
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C 87	15.2	76.0	124	16	US-10-085-783A-54284	Sequence 54284, A	160	15.2	76.0	57561	13	US-10-087-192-1129	Sequence 1129, Ap
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C 89	15.2	76.0	308	10	US-09-903-412-111	Sequence 111, App	162	15.2	76.0	196686	13	US-10-087-192-484	Sequence 484, App
C 90	15.2	76.0	308	15	US-10-174-171A-111	Sequence 111, App	163	15.2	76.0	267156	11	US-09-968-007A-427	Sequence 427, App
C 91	15.2	76.0	308	15	US-10-165-155-111	Sequence 111, App	164	15.2	76.0	378361	10	US-09-901-136-3	Sequence 3, Appli
C 92	15.2	76.0	308	15	US-10-130-162-111	Sequence 111, App	165	15.2	76.0	884973	9	US-09-263-959-1	Sequence 1, Appli
C 93	15.2	76.0	308	15	US-10-006-760-1	Sequence 1, Appli	166	15.2	76.0	2731748	17	US-10-297-465A-1	Sequence 1, Appli
C 94	15.2	76.0	344	16	US-10-424-599-895	Sequence 895, App	167	15.2	76.0	2731748	17	US-10-297-465A-1	Sequence 1, Appli
C 95	15.2	76.0	370	16	US-10-424-599-895	Sequence 895, App	168	15.2	76.0	2731748	17	US-10-297-465A-1	Sequence 1, Appli
C 96	15.2	76.0	398	16	US-10-424-599-118557	Sequence 118557, A	169	15.2	76.0	483	17	US-10-021-323-6495	Sequence 6495, Ap
C 97	15.2	76.0	412	10	US-09-918-995-15694	Sequence 15694, A	170	15.2	76.0	525	17	US-10-021-323-10247	Sequence 10247, A
C 98	15.2	76.0	412	10	US-09-918-995-33525	Sequence 33525, A	171	15.2	76.0	551	17	US-10-021-323-11169	Sequence 11169, A
C 99	15.2	76.0	416	10	US-09-918-995-4576	Sequence 4576, Ap	172	15.2	76.0	591	17	US-10-021-323-8167	Sequence 8167, Ap
C 100	15.2	76.0	428	13	US-10-027-632-294908	Sequence 294908, A	173	15.2	76.0	202	18	US-10-425-115-6165	Sequence 6165, Ap
C 101	15.2	76.0	428	13	US-10-027-632-294908	Sequence 294908, A	174	15.2	76.0	202	18	US-10-425-115-6165	Sequence 6165, Ap
C 102	15.2	76.0	604	13	US-10-027-632-261543	Sequence 261543, A	175	15.2	76.0	327	11	US-09-732-627A-4895	Sequence 4895, Ap
C 103	15.2	76.0	604	13	US-10-027-632-261543	Sequence 261543, A	176	15.2	76.0	406	10	US-09-918-995-10667	Sequence 10667, A
C 104	15.2	76.0	611	13	US-10-027-632-245805	Sequence 245805, A	177	15.2	76.0	415	15	US-10-172-118-2053	Sequence 2053, Ap
C 105	15.2	76.0	611	13	US-10-027-632-245805	Sequence 245805, A	178	15.2	76.0	415	15	US-10-172-118-2053	Sequence 2053, Ap
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C 113	15.2	76.0	663	15	US-10-006-760-16	Sequence 16, Appl	186	15.2	76.0	514	17	US-10-459-285-56	Sequence 56, Appl
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C 116	15.2	76.0	676	13	US-10-027-632-192838	Sequence 192838, A	189	15.2	76.0	555	9	US-09-917-800A-415	Sequence 415, App
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C 118	15.2	76.0	685	18	US-10-425-115-126973	Sequence 126973, A	191	15.2	76.0	602	17	US-10-198-846-10963	Sequence 10963, A
C 119	15.2	76.0	687	15	US-10-006-760-13	Sequence 13, Appl	192	15.2	76.0	618	14	US-10-198-846-8583	Sequence 8583, Ap
C 120	15.2	76.0	704	15	US-10-006-760-13	Sequence 13, Appl	193	15.2	76.0	657	17	US-10-198-846-8583	Sequence 8583, Ap
C 121	15.2	76.0	729	16	US-10-424-599-137002	Sequence 137002, A	194	15.2	76.0	751	17	US-10-767-701-9634	Sequence 9634, Ap
C 122	15.2	76.0	816	16	US-10-424-599-111069	Sequence 111069, A	195	15.2	76.0	761	13	US-10-027-632-149070	Sequence 149070, A
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C 125	15.2	76.0	1743	9	US-09-808-387-35	Sequence 35, Appl	198	15.2	76.0	796	15	US-10-027-632-153510	Sequence 153510, A
C 126	15.2	76.0	1809	16	US-10-282-122A-41609	Sequence 41609, A	199	15.2	76.0	821	17	US-10-437-963-8190	Sequence 8190, A
C 127	15.2	76.0	2180	13	US-10-027-632-102810	Sequence 102810, A	200	15.2	76.0	881	14	US-10-198-846-1662	Sequence 1662, Ap
C 128	15.2	76.0	2180	13	US-10-027-632-102811	Sequence 102811, A	201	15.2	76.0	953	16	US-10-260-228A-949	Sequence 949, App
C 129	15.2	76.0	2180	13	US-10-027-632-102811	Sequence 102811, A	202	15.2	76.0	987	16	US-10-282-122A-34998	Sequence 34998, A
C 130	15.2	76.0	2180	13	US-10-027-632-102811	Sequence 102811, A	203	15.2	76.0	1003	18	US-10-425-115-14194	Sequence 14194, A
C 131	15.2	76.0	2480	14	US-10-078-770-53	Sequence 53, Appl	204	15.2	76.0	1089	18	US-10-425-115-141832	Sequence 141832, A
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C 133	15.2	76.0	2581	15	US-10-001-885-26	Sequence 26, Appl	206	15.2	76.0	1142	9	US-09-738-626-596	Sequence 596, App
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C 135	15.2	76.0	3042	17	US-10-384-339C-2	Sequence 2, Appli	208	15.2	76.0	1467	16	US-10-425-114-10468	Sequence 10468, A
C 136	15.2	76.0	3118	17	US-10-437-963-96147	Sequence 96147, A	209	15.2	76.0	1541	16	US-10-374-780A-1767	Sequence 1767, Ap
C 137	15.2	76.0	3146	13	US-10-027-632-115032	Sequence 115032, A	210	15.2	76.0	1541	16	US-10-424-599-22294	Sequence 22294, A
C 138	15.2	76.0	3146	13	US-10-027-632-115032	Sequence 115032, A	211	15.2	76.0	1541	16	US-10-425-114-3868	Sequence 3868, Ap
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C 140	15.2	76.0	3705	9	US-09-764-877-2510	Sequence 2510, Ap	213	15.2	76.0	2000	9	US-09-887-576-125	Sequence 125, App
C 141	15.2	76.0	3705	16	US-10-424-515-2510	Sequence 2510, Ap	214	15.2	76.0	2085	10	US-09-846-589A-9	Sequence 9, Appli
C 142	15.2	76.0	3921	10	US-09-921-406C-29	Sequence 29, Appl	215	15.2	76.0	2085	18	US-10-796-667-9	Sequence 9, Appli
C 143	15.2	76.0	3921	15	US-10-007-926A-222	Sequence 222, App	216	15.2	76.0	2134	16	US-10-425-114-3372	Sequence 3372, Ap
C 144	15.2	76.0	3921	15	US-10-269-909-19	Sequence 19, Appl	217	15.2	76.0	2164	18	US-10-425-115-43534	Sequence 43534, A
C 145	15.2	76.0	3921	15	US-10-366-288-1	Sequence 1, Appli	218	15.2	76.0	2184	17	US-10-437-963-25255	Sequence 25255, A
C 146	15.2	76.0	3921	15	US-10-172-118-1036	Sequence 1036, Ap	219	15.2	76.0	2340	10	US-09-946-374-394	Sequence 394, App
C 147	15.2	76.0	3921	16	US-10-342-887-1036	Sequence 1036, Ap	220	15.2	76.0	2340	13	US-10-052-586-379	Sequence 379, App
C 148	15.2	76.0	3921	16	US-10-287-226-319	Sequence 319, App	221	15.2	76.0	2340	14	US-10-174-590-379	Sequence 379, App
C 149	15.2	76.0	3921	17	US-10-648-593-1	Sequence 1, Appli	222	15.2	76.0	2340	14	US-10-176-758-379	Sequence 379, App
C 150	15.2	76.0	5218	15	US-10-301-822-168	Sequence 168, App	223	15.2	76.0	2340	14	US-10-175-737-379	Sequence 379, App
C 151	15.2	76.0	9877	9	US-09-764-877-3944	Sequence 3944, Ap	224	15.2	76.0	2340	14	US-10-174-581-379	Sequence 379, App
C 152	15.2	76.0	9877	16	US-10-242-515-3944	Sequence 3944, Ap	225	15.2	76.0	2340	14	US-10-176-483-379	Sequence 379, App
C 153	15.2	76.0	10331	10	US-09-764-891-6032	Sequence 6032, Ap	226	15.2	76.0	2340	14	US-10-176-749-379	Sequence 379, App
C 154	15.2	76.0	14006	15	US-10-311-455-1931	Sequence 1931, Ap	227	15.2	76.0	2340	14	US-10-176-914-379	Sequence 379, App
C 155	15.2	76.0	25001	16	US-10-187-658A-11	Sequence 11, Appl	228	15.2	76.0	2340	14	US-10-176-915-379	Sequence 379, App
C 156	15.2	76.0	26392	13	US-10-087-192-199	Sequence 199, App	229	15.2	76.0	2340	14	US-10-173-706-379	Sequence 379, App
C 157	15.2	76.0	28616	16	US-10-455-552-1	Sequence 1, Appli	230	15.2	76.0	2340	14	US-10-175-738-379	Sequence 379, App
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C 699	14.8	74.0	2340	15	US-10-194-457-379	Sequence 379, App	C 772	14.8	74.0	2340	15	US-10-013-915A-394	Sequence 394, App
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C 701	14.8	74.0	2340	15	US-10-196-747-379	Sequence 379, App	C 774	14.8	74.0	2340	15	US-10-195-887-379	Sequence 379, App
C 702	14.8	74.0	2340	15	US-10-017-253A-394	Sequence 394, App	C 775	14.8	74.0	2340	15	US-10-195-893-379	Sequence 379, App
C 703	14.8	74.0	2340	15	US-10-173-689-379	Sequence 379, App	C 776	14.8	74.0	2340	15	US-10-179-509-379	Sequence 379, App
C 704	14.8	74.0	2340	15	US-10-173-690-379	Sequence 379, App	C 777	14.8	74.0	2340	15	US-10-194-486-379	Sequence 379, App
C 705	14.8	74.0	2340	15	US-10-173-691-379	Sequence 379, App	C 778	14.8	74.0	2340	15	US-10-198-500-379	Sequence 379, App
C 706	14.8	74.0	2340	15	US-10-173-694-379	Sequence 379, App	C 779	14.8	74.0	2340	15	US-10-198-506-379	Sequence 379, App
C 707	14.8	74.0	2340	15	US-10-173-698-379	Sequence 379, App	C 780	14.8	74.0	2340	15	US-10-205-506-379	Sequence 379, App
C 708	14.8	74.0	2340	15	US-10-173-699-379	Sequence 379, App	C 781	14.8	74.0	2340	15	US-10-174-570-379	Sequence 379, App
C 709	14.8	74.0	2340	15	US-10-173-707-379	Sequence 379, App	C 782	14.8	74.0	2340	15	US-10-183-005-379	Sequence 379, App
C 710	14.8	74.0	2340	15	US-10-174-569-379	Sequence 379, App	C 783	14.8	74.0	2340	15	US-10-179-523-379	Sequence 379, App
C 711	14.8	74.0	2340	15	US-10-174-583-379	Sequence 379, App	C 784	14.8	74.0	2340	15	US-10-199-463-379	Sequence 379, App
C 712	14.8	74.0	2340	15	US-10-174-587-379	Sequence 379, App	C 785	14.8	74.0	2340	15	US-10-202-471-379	Sequence 379, App
C 713	14.8	74.0	2340	15	US-10-174-589-379	Sequence 379, App	C 786	14.8	74.0	2340	15	US-10-015-390A-394	Sequence 394, App
C 714	14.8	74.0	2340	15	US-10-175-736-379	Sequence 379, App	C 787	14.8	74.0	2340	15	US-10-015-395A-394	Sequence 394, App
C 715	14.8	74.0	2340	15	US-10-175-742-379	Sequence 379, App	C 788	14.8	74.0	2340	15	US-10-011-795A-394	Sequence 394, App
C 716	14.8	74.0	2340	15	US-10-175-743-379	Sequence 379, App	C 789	14.8	74.0	2340	15	US-10-012-231A-394	Sequence 394, App
C 717	14.8	74.0	2340	15	US-10-175-744-379	Sequence 379, App	C 790	14.8	74.0	2340	15	US-10-197-709-379	Sequence 379, App
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C 719	14.8	74.0	2340	15	US-10-175-748-379	Sequence 379, App	C 792	14.8	74.0	2340	15	US-10-206-916-379	Sequence 379, App
C 720	14.8	74.0	2340	15	US-10-175-753-379	Sequence 379, App	C 793	14.8	74.0	2340	15	US-10-425-115-139810	Sequence 139810, A
C 721	14.8	74.0	2340	15	US-10-175-754-379	Sequence 379, App	C 794	14.8	74.0	2340	15	US-10-425-115-139810	Sequence 139810, A
C 722	14.8	74.0	2340	15	US-10-176-480-379	Sequence 379, App	C 795	14.8	74.0	2340	15	US-10-424-599-22293	Sequence 22293, A
C 723	14.8	74.0	2340	15	US-10-176-489-379	Sequence 379, App	C 796	14.8	74.0	2340	15	US-10-424-599-22293	Sequence 22293, A
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C 727	14.8	74.0	2340	15	US-10-176-920-379	Sequence 379, App	C 800	14.8	74.0	2340	15	US-10-015-395A-394	Sequence 394, App
C 728	14.8	74.0	2340	15	US-10-176-922-379	Sequence 379, App	C 801	14.8	74.0	2340	15	US-10-206-916-379	Sequence 379, App
C 729	14.8	74.0	2340	15	US-10-176-924-379	Sequence 379, App	C 802	14.8	74.0	2340	15	US-10-425-115-139810	Sequence 139810, A
C 730	14.8	74.0	2340	15	US-10-176-984-379	Sequence 379, App	C 803	14.8	74.0	2340	15	US-10-425-115-139810	Sequence 139810, A
C 731	14.8	74.0	2340	15	US-10-179-508-379	Sequence 379, App	C 804	14.8	74.0	2340	15	US-10-424-599-734	Sequence 394, App
C 732	14.8	74.0	2340	15	US-10-179-512-379	Sequence 379, App	C 805	14.8	74.0	2340	15	US-10-424-599-734	Sequence 394, App
C 733	14.8	74.0	2340	15	US-10-179-515-379	Sequence 379, App	C 806	14.8	74.0	2340	15	US-09-070-927A-286	Sequence 286, App
C 734	14.8	74.0	2340	15	US-10-173-692-379	Sequence 379, App	C 807	14.8	74.0	2340	15	US-10-384-398C-22	Sequence 22, Appl
C 735	14.8	74.0	2340	15	US-10-015-392A-394	Sequence 394, App	C 808	14.8	74.0	2340	15	US-10-384-398C-22	Sequence 22, Appl
C 736	14.8	74.0	2340	15	US-10-017-306A-394	Sequence 394, App	C 809	14.8	74.0	2340	15	US-10-120-988-235	Sequence 99, Appl
C 737	14.8	74.0	2340	15	US-10-173-703-379	Sequence 379, App	C 810	14.8	74.0	2340	15	US-10-757-262-99	Sequence 7, Appl
C 738	14.8	74.0	2340	15	US-10-173-703-379	Sequence 379, App	C 811	14.8	74.0	2340	15	US-10-768-158-7	Sequence 2, Appl
C 739	14.8	74.0	2340	15	US-10-173-704-379	Sequence 379, App	C 812	14.8	74.0	2340	15	US-10-648-593-2	Sequence 1, Appl
C 740	14.8	74.0	2340	15	US-10-174-574-379	Sequence 379, App	C 813	14.8	74.0	2340	15	US-10-863-573-1	Sequence 1, Appl
C 741	14.8	74.0	2340	15	US-10-176-486-379	Sequence 379, App	C 814	14.8	74.0	2340	15	US-10-863-573-1	Sequence 1, Appl
C 742	14.8	74.0	2340	15	US-10-176-490-379	Sequence 379, App	C 815	14.8	74.0	2340	15	US-10-027-632-175169	Sequence 175169, A



Sequence 133786, A  
Sequence 16610, A  
Sequence 2747, Ap  
Sequence 5120, Ap  
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Sequence 17929, A  
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Sequence 1356, Ap  
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Sequence 9692, Ap  
Sequence 175307, A  
Sequence 42126, A  
Sequence 42127, A  
Sequence 42126, A

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14.2 71.0 321 16 US-10-424-599-130289  
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14.2 71.0 321 16 US-10-027-632-42127  
14.2 71.0 321 16 US-10-027-632-42126

## ALIGNMENTS

RESULT 1  
US-10-050-189A-8  
; Sequence 8, Application US/10050189A  
; Publication No. US20020168656A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben, Berish  
; APPLICANT: Anderson, Sylvia  
; TITLE OF INVENTION: Detection of Mutations in a Gene Encoding IKB Kinase-Complex-Associated With  
; TITLE OF INVENTION: Protein to Diagnose Familial Dysautonomia  
; FILE REFERENCE: Rubin 201  
; CURRENT APPLICATION NUMBER: US/10/050,189A  
; CURRENT FILING DATE: 2002-01-16  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-050-189A-8

Query Match 100.0%; Score 20; DB 13; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.7; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGTTAATCGAGAGTGCT 20  
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Db 1 GCAGTTAATCGAGAGTGCT 20

RESULT 2  
US-10-041-856-1  
; Sequence 1, Application US/10041856  
; Publication No. US20020169299A1  
; GENERAL INFORMATION:  
; APPLICANT: SLAUGENHAUPT, SUSAN  
; APPLICANT: GUSELLA, JAMES F.  
; TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL  
; TITLE OF INVENTION: DYSAUTONOMIA  
; FILE REFERENCE: 1829-4004US1  
; CURRENT APPLICATION NUMBER: US/10/041,856  
; CURRENT FILING DATE: 2002-07-08  
; PRIOR APPLICATION NUMBER: 60/260,080  
; PRIOR FILING DATE: 2001-01-06  
; NUMBER OF SEQ ID NOS: 88  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 66479  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-041-856-1

Query Match 100.0%; Score 20; DB 13; Length 66479;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGTTAATCGAGAGTGCT 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 33581 GCAGTTAATCGAGAGTGCT 33600

RESULT 3  
US-10-437-963-65936  
; Sequence 65936, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 65936  
; LENGTH: 2298  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MET4530\_66935C.1  
US-10-437-963-65936

Query Match 85.0%; Score 17; DB 17; Length 2298;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAGTTAATCGAGAGTGCT 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1627 CAGTTAATCGAGAGTGCT 1643

RESULT 4  
US-10-027-632-275091/c  
; Sequence 275091, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; POLYMERASIS: Polymorphisms in the Human Genome

; FILE REFERENCE: 10827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 275091

; LENGTH: 565

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-275091

Query Match 84.0%; Score 16.8; DB 13; Length 565;

Best Local Similarity 90.0%; Pred. No. 1.9e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAGTTAATGGAGAGTGGCT 20

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Db 529 GCAGTTAATGGAGAGTGGCT 510

RESULT 5

US-10-027-632-275091/c

; Sequence 275091, Application US/10027632

; Publication No. US20030204075A9

; GENERAL INFORMATION:

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; POLYMERASIS: Polymorphisms in the Human Genome

; FILE REFERENCE: 10827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 275091

; LENGTH: 565

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-275091

Query Match 84.0%; Score 16.8; DB 15; Length 565;

Best Local Similarity 90.0%; Pred. No. 1.9e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20  
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Db 1220 GCTGTTAATGGAGAGTGGCT 1239

## RESULT 8

US-10-424-599-116085/c  
; Sequence 116085, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 116085  
; LENGTH: 1965  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_75835C.1  
US-10-424-599-116085

Query Match 84.0%; Score 16.8; DB 16; Length 1965;  
Best Local Similarity 90.0%; Pred. No. 2.1e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20  
|||  
Db 1295 GCAGTTAATGGAGAGTGGCT 1276

## RESULT 9

US-09-873-367C-229  
; Sequence 229, Application US/09873367C  
; Publication No. US20030165839A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, Paul  
; APPLICANT: Soppet, Daniel  
; APPLICANT: Andrews, Gregory  
; APPLICANT: Augustus, Meena  
; APPLICANT: Ebner, Reinhard  
; APPLICANT: Carter, Kenneth  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using  
; FILE OF INVENTION: Signature Gene Sets  
; FILE REFERENCE: 689290-64  
; CURRENT APPLICATION NUMBER: US/09/873,367C  
; CURRENT FILING DATE: 2003-04-29  
; PRIOR APPLICATION NUMBER: U.S. 60/236,891  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: U.S. 60/236,842  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: U.S. 60/244,867  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR APPLICATION NUMBER: U.S. 60/245,084  
; PRIOR FILING DATE: 2000-11-01  
; NUMBER OF SEQ ID NOS: 1067  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 229  
; LENGTH: 4977  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-873-367C-229

Query Match 84.0%; Score 16.8; DB 10; Length 4977;  
Best Local Similarity 90.0%; Pred. No. 2.3e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20  
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Db 4806 GCTGTTAATGGAGAGTGGCT 4825

## RESULT 10

US-10-755-889-63  
; Sequence 63, Application US/10755889  
; Publication No. US20040171823A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB  
; TITLE OF INVENTION: PATHWAY  
; FILE REFERENCE: D0284 NP  
; CURRENT APPLICATION NUMBER: US/10/755,889  
; CURRENT FILING DATE: 2004-01-13  
; PRIOR APPLICATION NUMBER: U.S. 60/440,068  
; PRIOR FILING DATE: 2003-01-14  
; PRIOR APPLICATION NUMBER: U.S. 60/469,757  
; PRIOR FILING DATE: 2003-05-12  
; NUMBER OF SEQ ID NOS: 823  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 63  
; LENGTH: 4977  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-755-889-63

Query Match 84.0%; Score 16.8; DB 17; Length 4977;  
Best Local Similarity 90.0%; Pred. No. 2.3e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20  
|||  
Db 4806 GCTGTTAATGGAGAGTGGCT 4825

## RESULT 11

US-09-853-386-57  
; Sequence 57, Application US/09853386  
; Patent No. US20020049151A1  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Evelyn  
; APPLICANT: Bresnihan, Barry  
; APPLICANT: Conneely, Orla  
; APPLICANT: Fitzgerald, Oliver  
; TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR  
; FILE OF INVENTION: Subfamily of Nuclear Transcription Factors  
; FILE REFERENCE: P01972US1  
; CURRENT APPLICATION NUMBER: US/09/853,386  
; CURRENT FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: US 60/203645  
; PRIOR FILING DATE: 2000-05-12  
; NUMBER OF SEQ ID NOS: 153  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 57  
; LENGTH: 5115  
; TYPE: DNA  
; ORGANISM: Sus scrofa  
US-09-853-386-57

Query Match 84.0%; Score 16.8; DB 9; Length 5115;  
Best Local Similarity 90.0%; Pred. No. 2.3e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20  
|||  
Db 4908 GCTGTTAATGGAGAGTGGCT 4927

## RESULT 12



```
US-10-414-080-8
; Sequence 8, Application US/10414080
; Publication No. US2003020288A1
; GENERAL INFORMATION:
; APPLICANT: MULLICAN, SHANNON E.
; APPLICANT: CONNELLY, ORLA M.
; APPLICANT: MILBRANDT, JEFFREY
; TITLE OF INVENTION: NOR-1 AND NUR77 NUCLEAR RECEPTORS AS TARGETS FOR
; FILE REFERENCE: P02454US1
; CURRENT APPLICATION NUMBER: US/10/414,080
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 60/373,238
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 5115
; TYPE: DNA
; ORGANISM: Sus scrofa
US-10-414-080-8

Query Match      84.0%; Score 16.8; DB 15; Length 5115;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCAGTTAATGGAGAGTGGCT 20
Db      4908 GCTGTTAATGGAGAGTGGCT 4927
|||||

RESULT 13
US-09-529-063-59
; Sequence 59, Application US/09529063
; Patent No. US20020102542A1
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, DAIKICHI
; APPLICANT: SHIBAYAMA, SHIRO
; APPLICANT: TADA, HIDEAKI
; TITLE OF INVENTION: POLYPEPTIDE, cDNA ENCODING THE POLYPEPTIDE, AND USE OF
; FILE REFERENCE: Q58769
; CURRENT APPLICATION NUMBER: US/09/529,063
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: PCT/JP98/04514
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: JP 9-274674
; PRIOR FILING DATE: 1997-10-07
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 5178
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-529-063-59

Query Match      84.0%; Score 16.8; DB 9; Length 5178;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCAGTTAATGGAGAGTGGCT 20
Db      3291 GCAGTCAATGGAGAGTGGCT 3310
|||||

RESULT 14
US-10-414-378-59
; Sequence 59, Application US/10414378
; Publication No. US20030165981A1
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, DAIKICHI
; APPLICANT: SHIBAYAMA, SHIRO
; APPLICANT: TADA, HIDEAKI
```

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US-10-414-378-59
; TITLE OF INVENTION: POLYPEPTIDE, cDNA ENCODING THE POLYPEPTIDE, AND USE OF
; FILE REFERENCE: Q58769
; CURRENT APPLICATION NUMBER: US/10/414,378
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US/09/529,063
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: PCT/JP98/04514
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: JP 9-274674
; PRIOR FILING DATE: 1997-10-07
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 5178
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-414-378-59

Query Match      84.0%; Score 16.8; DB 15; Length 5178;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCAGTTAATGGAGAGTGGCT 20
Db      3291 GCAGTCAATGGAGAGTGGCT 3310
|||||

RESULT 15
US-09-529-063-60
; Sequence 60, Application US/09529063
; Patent No. US20020102542A1
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, DAIKICHI
; APPLICANT: SHIBAYAMA, SHIRO
; APPLICANT: TADA, HIDEAKI
; TITLE OF INVENTION: POLYPEPTIDE, cDNA ENCODING THE POLYPEPTIDE, AND USE OF
; FILE REFERENCE: Q58769
; CURRENT APPLICATION NUMBER: US/09/529,063
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: PCT/JP98/04514
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: JP 9-274674
; PRIOR FILING DATE: 1997-10-07
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 5457
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (8)..(46)
; NAME/KEY: mat_peptide
; LOCATION: (47)..(5185)
; NAME/KEY: CDS
; LOCATION: (8)..(5185)
US-09-529-063-60

Query Match      84.0%; Score 16.8; DB 9; Length 5457;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCAGTTAATGGAGAGTGGCT 20
Db      3298 GCAGTCAATGGAGAGTGGCT 3317
|||||

RESULT 16
US-10-414-378-60
; Sequence 60, Application US/10414378
; Publication No. US20030165981A1
```



```

; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1313
; LENGTH: 29220
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-868-1313

Query Match      84.0%; Score 16.8; DB 9; Length 29220;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAGTTAATGGAGAGTGGCT 20
   |||||
Db 9230 GCGGTAATGGAGAGTGGCT 9249
   |||||

RESULT 23
US-10-087-192-661
; Sequence 661, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 661
; LENGTH: 55404
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(55404)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-661

Query Match      84.0%; Score 16.8; DB 13; Length 55404;
Best Local Similarity 90.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAGTTAATGGAGAGTGGCT 20
   |||||
Db 33849 GCGGTAATGGAGAGTGGCT 33868
   |||||

RESULT 24
US-09-795-668-1/c
; Sequence 1, Application US/09795668
; Patent No. US20020045577A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinhorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUWAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/795,668
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; FILE REFERENCE: PT232

US-10-014-814-5
; Sequence 5, Application US/10014814
; Publication No. US20030032058A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Cimborra, Daniel M.
; APPLICANT: Heichman, Karen
; APPLICANT: Bartel, Paul L.
; TITLE OF INVENTION: Protein-Protein Interactions
; FILE REFERENCE: 2318-277-11
; CURRENT APPLICATION NUMBER: US/10/014,814
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/255,063
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 8490
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (162)..(6584)
US-10-014-814-5

Query Match      84.0%; Score 16.8; DB 14; Length 8490;
Best Local Similarity 90.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAGTTAATGGAGAGTGGCT 20
   |||||
Db 4697 GCGGTAATGGAGAGTGGCT 4716
   |||||

RESULT 21
US-09-764-868-1312/c
; Sequence 1312, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1312
; LENGTH: 29220
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-868-1312

Query Match      84.0%; Score 16.8; DB 9; Length 29220;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAGTTAATGGAGAGTGGCT 20
   |||||
Db 19991 GCGGTAATGGAGAGTGGCT 19972
   |||||

RESULT 22
US-09-764-868-1313
; Sequence 1313, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
```

```
; SEQ ID NO 1
; LENGTH: 1503841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: r=g or a
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: y=t/u or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: m=a or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: w=a or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: k=g or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: s=g or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: d=a or g or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: h=a or c or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: v=a or g or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: n=a or g or c or t/u
; US-09-795-686-1

Query Match      84.0%; Score 16.8; DB 9; Length 1503841;
Best Local Similarity 90.0%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGCT 20
   ||| ||||| ||||| ||||| |||||
DB 453558 GCAAGTAATGGAGAGTGCT 453539

RESULT 26
US-09-795-686-1/c
; Sequence 1, Application US/09795686
; Patent No. US20020094954A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2005-001
; CURRENT APPLICATION NUMBER: US/09/795,686
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,715
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1503841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: r=g or a
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: y=t/u or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: m=a or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: w=a or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: k=g or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: s=g or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: d=a or g or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: h=a or c or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: v=a or g or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: n=a or g or c or t/u
; US-09-795-686-1

Query Match      84.0%; Score 16.8; DB 9; Length 1503841;
Best Local Similarity 90.0%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGCT 20
   ||| ||||| ||||| ||||| |||||
DB 453558 GCAAGTAATGGAGAGTGCT 453539

RESULT 25
US-09-795-686-1/c
; Sequence 1, Application US/09795686
; Patent No. US20020094954A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2005-001
; CURRENT APPLICATION NUMBER: US/09/795,686
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,715
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1503841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: r=g or a
```

```

; LOCATION: (1)...(1531)
; OTHER INFORMATION: m=a or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: k=g or t/u
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: s=g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: w=a or t/u
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: b=g or c or t/u
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: d=a or g or t/u
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: h=a or c or t/u
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: v=a or g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: n=a or g or c or t/u
; OTHER INFORMATION: n may be a, c, g, or t.
US-09-946-807-1

Query Match      84.0%; Score 16.8; DB 9; Length 1503841;
Best Local Similarity 90.0%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAGTTAATGGAGAGTGGCT 20
Db 453558 GCAAGTAATGGAGAGTGGCT 453539

RESULT 27
US-09-747-810-1
; Sequence 1, Application US/09747810
; Patent No. US20020012903A1
; GENERAL INFORMATION:
; APPLICANT: Goldman, Steven A.
; TITLE OF INVENTION: A METHOD FOR ISOLATING AND PURIFYING MULTIPOTENTIAL NEURAL PROGEN
; FILE REFERENCE: 19603/3580
; CURRENT APPLICATION NUMBER: US/09/747,810
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/173,003
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 52216
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-747-810-1

Query Match      82.0%; Score 15.4; DB 9; Length 52216;
Best Local Similarity 94.4%; Pred. No. 4.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAGTTAATGGAGAGTGG 18
Db 21276 GCAGTTAATGGAGAGTGG 21293
```

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US-10-240-466-1
; Sequence 1, Application US/10240466
; Publication No. US20030175941A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human Serine Racemase Enzyme
; FILE REFERENCE: LIO115-US
; CURRENT APPLICATION NUMBER: US/10/240,466
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/EP01/03668
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,748
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/194,249
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1336
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1336)
; OTHER INFORMATION: n may be a, c, g, or t.
US-10-240-466-1

Query Match      80.0%; Score 16; DB 15; Length 1336;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTAATGGAGAGTGGCT 20
Db 1166 TTAATGGAGAGTGGCT 1181

RESULT 29
US-09-789-300A-1
; Sequence 1, Application US/09789300A
; Publication No. US20020115137A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: 22406, A No. 6458576e1 Human Pyridoxal-Phosphate
; FILE REFERENCE: 35800/208926
; CURRENT APPLICATION NUMBER: US/09/789,300A
; CURRENT FILING DATE: 2001-02-20
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1770
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(1091)
US-09-789-300A-1

Query Match      80.0%; Score 16; DB 9; Length 1770;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTAATGGAGAGTGGCT 20
Db 1183 TTAATGGAGAGTGGCT 1198
```

```
RESULT 30
US-10-164-966-1
; Sequence 1, Application US/10164966
; Publication No. US20030064439A1
; GENERAL INFORMATION:
; APPLICANT: Bandaru, Rajasekhkar
; APPLICANT: Glucksman, Maria Alexandra
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Encoding Melanoma
; TITLE OF INVENTION: Associated Antigen Molecules, Aminotransferase
; TITLE OF INVENTION: Molecules, ATPase Molecules, Acyltransferase Molecules,
; TITLE OF INVENTION: Pyridoxal-Phosphate Dependant Enzyme Molecules and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/247400
; CURRENT APPLICATION NUMBER: US/10/164,966
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 10/034,864
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/258,517
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 09/996,194
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/250,348
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/250,073
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/253,878
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,338
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/908,928
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/220,455
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 09/908,180
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/219,740
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 09/887,389
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/214,138
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/789,300
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/183,208
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1770
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(1091)
US-10-164-966-1

Query Match      80.0%; Score 16; DB 14; Length 1770;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5      TTAATGGAGAGTGGCT 20
DB      1183  TTAATGGAGAGTGGCT 1198
|||||
RESULT 31
US-10-311-455-42
; Sequence 42, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
```

```
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013,1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 42
; LENGTH: 12460
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-42

Query Match      80.0%; Score 16; DB 15; Length 12460;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3      AGTTAATGGAGAGTGG 18
DB      4182  AGTTAATGGAGAGTGG 4197
|||||
RESULT 32
US-10-674-124A-18004
; Sequence 18004, Application US/10674124A
; Publication No. US20040197797A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: TAMIYA, Gen
; TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE
; FILE REFERENCE: ORIN-003CIP
; CURRENT APPLICATION NUMBER: US/10/674,124A
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 10/257,511
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/JP00/07621
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: JP2000-112699
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: JP2002-327516
; PRIOR FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: JP2002-383869
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 27110
; SEQ ID NO 18004
; LENGTH: 250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: D11S1327
; FEATURE:
; OTHER INFORMATION: Located on chromosome 11
; FEATURE:
; OTHER INFORMATION: Distance between a terminus base of telomere on
; OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base
; OTHER INFORMATION: sequence : 119371886
; FEATURE:
; OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
; OTHER INFORMATION: sequence listing upward to telomere on chromosomal short arm and
; OTHER INFORMATION: 5'-terminus of this base sequence : 68187
US-10-674-124A-18004

Query Match      79.0%; Score 15.8; DB 18; Length 250;
```

Best Local Similarity 89.5%; Pred. No. 5.6e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGGC 20  
Db 178 CAGTAGTGGAGAGTGGC 196

RESULT 33

US-09-783-590-4359/c  
; Sequence 4359, Application US/09783590  
; Patent No. US20020110850A1  
; GENERAL INFORMATION:  
; APPLICANT: Dillon, Patrick J.  
; APPLICANT: Haseltine, William A.  
; APPLICANT: Li, Haodong  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2  
; FILE REFERENCE: PO-16.2C1  
; CURRENT APPLICATION NUMBER: US/09/783,590  
; CURRENT FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 08/420,856  
; PRIOR FILING DATE: 1995-04-12  
; PRIOR APPLICATION NUMBER: 08/346,731  
; PRIOR FILING DATE: 1994-11-21  
; NUMBER OF SEQ ID NOS: 12485  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 4359  
; LENGTH: 334  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (18)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (19)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (42)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (111)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (154)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (227)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (268)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (290)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (296)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (307)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (311)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (319)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (321)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-783-590-4359

Query Match 79.0%; Score 15.8; DB 9; Length 334;  
Best Local Similarity 89.5%; Pred. No. 5.8e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGC 19  
Db 101 GCAGTTAATGGAGAGTGGC 83

RESULT 34

US-10-424-599-142382/c  
; Sequence 142382, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 142382  
; LENGTH: 548  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(548)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MBT3847\_99587C.1  
US-10-424-599-142382

Query Match 79.0%; Score 15.8; DB 16; Length 548;  
Best Local Similarity 89.5%; Pred. No. 6e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGC 19  
Db 30 GCAGTTAATGGAGAGTGGC 12

RESULT 35

US-10-027-632-171253/c  
; Sequence 171253, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; POLYMORPHISMS IN THE HUMAN GENOME  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 171253  
; LENGTH: 856  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-171253

Query Match 79.0%; Score 15.8; DB 13; Length 856;  
Best Local Similarity 89.5%; Pred. No. 6.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGGCT 20  
Db 595 CAGTTAATGGAGAGTGGCT 577

## RESULT 36

US-10-027-632-171253/c  
; Sequence 171253, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827,129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; PRIORITY FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 171253

; LENGTH: 856  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-171253

Query Match 79.0%; Score 15.8; DB 15; Length 856;  
Best Local Similarity 89.5%; Pred. No. 6.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGGCT 20  
Db 595 CAGTTAATGGAGAGTGGCT 577

## RESULT 37

US-10-007-280A-125/c  
; Sequence 125, Application US/10007280A  
; Publication No. US20030059784A1  
; GENERAL INFORMATION:

; APPLICANT: Sun, Yongming  
; APPLICANT: Recipon, Herve  
; APPLICANT: Salceda, Susana  
; APPLICANT: Chenghua, Liu

; TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Pro  
; CURRENT APPLICATION NUMBER: US/10/007,280A  
; PRIORITY FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: US 60/246,640  
; PRIOR FILING DATE: 2000-11-08  
; NUMBER OF SEQ ID NOS: 238

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 125  
; LENGTH: 896  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-007-280A-125

Query Match 79.0%; Score 15.8; DB 14; Length 896;  
Best Local Similarity 89.5%; Pred. No. 6.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGGCT 20  
Db 511 CAGTTAATGGAGAGTGGCT 493

## RESULT 38

US-10-007-280A-126/c  
; Sequence 126, Application US/10007280A  
; Publication No. US20030059784A1  
; GENERAL INFORMATION:

; APPLICANT: Sun, Yongming  
; APPLICANT: Recipon, Herve  
; APPLICANT: Salceda, Susana  
; APPLICANT: Chenghua, Liu

; TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Prot  
; FILE REFERENCE: DEX-0257  
; CURRENT APPLICATION NUMBER: US/10/007,280A  
; PRIORITY FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: US 60/246,640  
; PRIOR FILING DATE: 2000-11-08  
; NUMBER OF SEQ ID NOS: 238  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 126  
; LENGTH: 998  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-007-280A-126

Query Match 79.0%; Score 15.8; DB 14; Length 998;  
Best Local Similarity 89.5%; Pred. No. 6.3e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGGCT 20  
Db 511 CAGTTAATGGAGAGTGGCT 493

## RESULT 39

US-10-437-963-47072  
; Sequence 47072, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; PRIORITY FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 47072  
; LENGTH: 1155  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_49877C.1





```
QY      2 CAGTTAATGGAGAGTGGCT 20
      ||||| ||||| ||||| |||||
Db      3404 CAGTCAATGGAGAGGGGCT 3422

RESULT 43
US-09-764-891-6452
; Sequence 6452, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6452
; LENGTH: 18820
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-6452

Query Match      79.0%; Score 15.8; DB 10; Length 18820;
Best Local Similarity 89.5%; Pred. No. 7.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CAGTTAATGGAGAGTGGCT 20
      ||||| ||||| ||||| |||||
Db      862 CAGTCAATGGAGAGTGGCT 880

RESULT 44
US-10-205-428-733
; Sequence 733, Application US/10205428
; Publication No. US20030108907A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA117C1
; CURRENT APPLICATION NUMBER: US/10/205,428
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 09/764,892
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1019
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 733
; LENGTH: 18820
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-428-733

Query Match      79.0%; Score 15.8; DB 15; Length 18820;
Best Local Similarity 89.5%; Pred. No. 7.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CAGTTAATGGAGAGTGGCT 20
      ||||| ||||| ||||| |||||
Db      862 CAGTCAATGGAGAGTGGCT 880

RESULT 45
US-09-764-891-6454
; Sequence 6454, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6454
; LENGTH: 32191
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-6454

Query Match      79.0%; Score 15.8; DB 10; Length 32191;
Best Local Similarity 89.5%; Pred. No. 8.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CAGTTAATGGAGAGTGGCT 20
      ||||| ||||| ||||| |||||
Db      9913 CAGTCAATGGAGAGTGGCT 9931

RESULT 46
US-10-205-428-735
; Sequence 735, Application US/10205428
; Publication No. US20030108907A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA117C1
; CURRENT APPLICATION NUMBER: US/10/205,428
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 09/764,892
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1019
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 735
; LENGTH: 32191
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-428-735

Query Match      79.0%; Score 15.8; DB 15; Length 18820;
Best Local Similarity 89.5%; Pred. No. 7.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

US-10-205-428-735

Query Match 79.0%; Score 15.8; DB 15; Length 32191;  
Best Local Similarity 89.5%; Pred. No. 8.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGGCT 20  
||| ||||| ||||| |||||  
Db 9913 CAGTCATGGAGATGGCT 9931

RESULT 47

US-10-087-192-1579  
; Sequence 1579, Application US/10087192  
; Publication No. US20020182586A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.  
; APPLICANT: Engelhard, Eric K.  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR  
; FILE REFERENCE: 529452000122  
; CURRENT APPLICATION NUMBER: US/10/087,192  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 09/747,377  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/798,586  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 2059  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1579  
; LENGTH: 41554  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(41554)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-087-192-1579

Query Match 79.0%; Score 15.8; DB 13; Length 41554;  
Best Local Similarity 89.5%; Pred. No. 8.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGGCT 20  
||| ||||| ||||| |||||  
Db 36926 CAGTCATGGAGATGGCT 36944

RESULT 48

US-10-087-192-547/c  
; Sequence 547, Application US/10087192  
; Publication No. US20020182586A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.  
; APPLICANT: Engelhard, Eric K.  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR  
; FILE REFERENCE: 529452000122  
; CURRENT APPLICATION NUMBER: US/10/087,192  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 09/747,377  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/798,586  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 2059  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 547  
; LENGTH: 116858  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(116858)

; OTHER INFORMATION: n = A,T,C or G  
US-10-087-192-547

Query Match 79.0%; Score 15.8; DB 13; Length 116858;  
Best Local Similarity 89.5%; Pred. No. 9e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGGCT 20  
||| ||||| ||||| |||||  
Db 14148 CAGTCATGGAGATGGCT 14130

RESULT 49

US-10-085-117-283  
; Sequence 283, Application US/10085117  
; Publication No. US2003023234A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.  
; APPLICANT: Engelhard, Eric K.  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER  
; FILE REFERENCE: 529452000121  
; CURRENT APPLICATION NUMBER: US/10/085,117  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: US 09/798,586  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 361  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 283  
; LENGTH: 155579  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (1)...(155579)  
; OTHER INFORMATION: n = any nucleotide  
US-10-085-117-283

Query Match 79.0%; Score 15.8; DB 15; Length 155579;  
Best Local Similarity 89.5%; Pred. No. 9.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGGCT 20  
||| ||||| ||||| |||||  
Db 36816 CAGTTAATGGATATGGCT 36834

RESULT 50

US-09-783-590-6294  
; Sequence 6294, Application US/09783590  
; Patent No. US20020110850A1  
; GENERAL INFORMATION:  
; APPLICANT: Dillon, Patrick J.  
; APPLICANT: Haseltine, William A.  
; APPLICANT: Li, Haodong  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2  
; FILE REFERENCE: PO-16.2C1  
; CURRENT APPLICATION NUMBER: US/09/783,590  
; CURRENT FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 08/420,856  
; PRIOR FILING DATE: 1995-04-12  
; PRIOR APPLICATION NUMBER: 08/346,731  
; PRIOR FILING DATE: 1994-11-21  
; NUMBER OF SEQ ID NOS: 12485  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6294  
; LENGTH: 295  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (5)

```

; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (121)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (122)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (177)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (225)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (228)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (247)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (257)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (277)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (282)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (291)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-6294

```

```

Query Match          77.0%; Score 15.4; DB 9; Length 295;
Best Local Similarity 88.9%; Pred. No. 9e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

```

```

Qy      1 GCAGTTAATGGAGAGTGG 18
         |||||
Db      210 GCAGTGAATGGAGAGNGG 227

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Search completed: December 3, 2004, 07:43:26  
Job time : 1790.58 secs

GenCore version 5.1.6  
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Run on: December 3, 2004, 01:45:05 ; Search time 66.3158 Seconds  
(without alignments)  
214.365 Million cell updates/sec

Title: US-10-050-189A-8

Perfect score: 20

Sequence: 1 gcagtaatggagagtggct 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

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1: /cgn2\_6/ptodata/1/ina/5A COMB.seq.\*  
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# SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	16	80.0	1770	4	US-09-789-300A-1
2	15.8	79.0	318	4	US-09-328-352-21
3	15.8	79.0	351	4	US-09-328-352-24
4	15.8	79.0	2369	3	US-09-302-769-20
5	15.8	79.0	4335	3	US-09-058-489-19
6	15.8	79.0	4931	3	US-09-058-489-20
7	15.8	79.0	6476	3	US-09-058-489-21
8	15.4	77.0	1122	3	US-09-237-357-38
9	15.4	77.0	5044	4	US-09-735-935-3
10	15.4	77.0	5044	4	US-10-162-639-3
11	15.4	77.0	7151	4	US-09-839-477-7
12	15.4	77.0	9916	4	US-09-816-095-3
13	15.4	77.0	392000	4	US-10-027-983-11
14	15.2	76.0	35	4	US-09-638-202A-21
15	15.2	76.0	35	4	US-09-096-749A-21
16	15.2	76.0	35	4	US-09-637-614-21
17	15.2	76.0	308	4	US-09-638-202A-111
18	15.2	76.0	308	4	US-09-096-749A-111
19	15.2	76.0	308	4	US-09-637-614-111
20	15.2	76.0	1170	3	US-09-689-421-20
21	15.2	76.0	1170	3	US-09-389-528-20
22	15.2	76.0	1170	3	US-09-181-827A-20
23	15.2	76.0	1305	4	US-09-489-039A-4503
24	15.2	76.0	1332	4	US-09-489-039A-3898
25	15.2	76.0	2590	4	US-09-799-451-771
26	15.2	76.0	3566	3	US-08-689-421-32
27	15.2	76.0	3566	3	US-09-389-528-32

c 28	15.2	76.0	3566	3	US-09-181-827A-32	Sequence 32, Appl
c 29	15.2	76.0	5009	3	US-08-978-741-7	Sequence 7, Appl
c 30	15.2	76.0	5009	3	US-09-333-729A-8	Sequence 8, Appl
c 31	15	75.0	240	4	US-09-248-796A-6732	Sequence 6732, Ap
32	14.8	74.0	438	4	US-09-513-999C-1833	Sequence 1833, Ap
33	14.8	74.0	543	4	US-09-976-594-432	Sequence 432, App
34	14.8	74.0	867	4	US-09-248-796A-5837	Sequence 5837, Ap
35	14.8	74.0	1734	3	US-09-486-382B-1	Sequence 1, Appl
36	14.8	74.0	1734	3	US-09-486-382B-12	Sequence 12, Appl
37	14.8	74.0	1815	4	US-09-134-000C-1851	Sequence 1851, Ap
38	14.8	74.0	2085	3	US-09-352-990-9	Sequence 9, Appl
39	14.8	74.0	2962	2	US-08-449-645A-10	Sequence 10, Appl
40	14.8	74.0	2962	5	PCT-US95-04681-10	Sequence 10, Appl
41	14.8	74.0	2962	5	US-08-702-367A-10	Sequence 10, Appl
42	14.8	74.0	3150	4	US-09-186-350-23	Sequence 23, Appl
c 43	14.8	74.0	3611	2	US-08-727-118-1	Sequence 1, Appl
c 44	14.8	74.0	3669	4	US-09-774-528-335	Sequence 235, App
45	14.8	74.0	4049	1	US-08-162-809-17	Sequence 17, Appl
46	14.8	74.0	4097	1	US-08-162-809-11	Sequence 11, Appl
47	14.8	74.0	4698	4	US-09-895-652A-1	Sequence 1, Appl
48	14.8	74.0	5749	4	US-09-262-537-48	Sequence 48, Appl
49	14.8	74.0	3446	3	US-09-103-330-35	Sequence 35, Appl
c 50	14.8	74.0	37895	1	US-08-375-709-1	Sequence 1, Appl
c 51	14.8	74.0	37895	1	US-08-752-929-1	Sequence 1, Appl
c 52	14.8	74.0	37895	3	US-09-090-793-1	Sequence 1, Appl
c 53	14.8	74.0	37895	4	US-09-231-899-1	Sequence 1, Appl
c 54	14.8	74.0	70000	4	US-09-851-896-3	Sequence 3, Appl
c 55	14.8	74.0	1664976	4	US-08-916-421B-1	Sequence 1, Appl
c 56	14.8	74.0	1664976	4	US-09-892-570-1	Sequence 1, Appl
c 57	14.4	72.0	286	4	US-09-313-294A-5943	Sequence 5943, Ap
c 58	14.4	72.0	6111	3	US-09-538-414-9	Sequence 9, Appl
c 59	14.4	72.0	6111	3	US-10-074-279-9	Sequence 9, Appl
c 60	14.4	72.0	12949	3	US-09-538-414-11	Sequence 11, Appl
c 61	14.4	72.0	12949	4	US-10-074-279-11	Sequence 11, Appl
c 62	14.2	71.0	208	1	US-07-670-611-18	Sequence 18, Appl
63	14.2	71.0	208	1	US-08-220-674-18	Sequence 18, Appl
64	14.2	71.0	208	1	US-08-445-186-18	Sequence 18, Appl
65	14.2	71.0	208	1	US-08-446-549-18	Sequence 18, Appl
66	14.2	71.0	208	2	US-08-446-550-18	Sequence 18, Appl
67	14.2	71.0	234	4	US-09-107-532A-1858	Sequence 1858, Ap
68	14.2	71.0	241	4	US-09-702-705-988	Sequence 988, App
69	14.2	71.0	241	4	US-09-736-457-988	Sequence 988, App
70	14.2	71.0	241	4	US-09-614-124B-988	Sequence 988, App
71	14.2	71.0	241	4	US-09-671-325-988	Sequence 988, App
72	14.2	71.0	241	4	US-09-658-824-988	Sequence 988, App
73	14.2	71.0	279	4	US-09-603-552-9	Sequence 9, Appl
74	14.2	71.0	281	4	US-09-513-999C-34835	Sequence 34835, A
c 75	14.2	71.0	290	4	US-09-513-999C-20969	Sequence 20969, A
c 76	14.2	71.0	323	4	US-09-603-552-11	Sequence 11, Appl
c 77	14.2	71.0	348	4	US-09-308-246C-1	Sequence 1, Appl
c 78	14.2	71.0	366	3	US-09-171-962-1	Sequence 1, Appl
c 79	14.2	71.0	366	4	US-09-171-962-1	Sequence 1, Appl
c 80	14.2	71.0	369	4	US-09-489-039A-1400	Sequence 1400, Ap
c 81	14.2	71.0	389	4	US-09-513-999C-26192	Sequence 26192, A
c 82	14.2	71.0	393	2	US-08-944-449-1	Sequence 1, Appl
c 83	14.2	71.0	393	3	US-09-353-362-1	Sequence 1, Appl
c 84	14.2	71.0	434	4	US-09-270-767-306	Sequence 306, Ap
c 85	14.2	71.0	434	4	US-09-270-767-18588	Sequence 18588, Ap
c 86	14.2	71.0	732	4	US-09-248-796A-5294	Sequence 5294, Ap
c 87	14.2	71.0	817	4	US-09-270-767-3132	Sequence 3132, Ap
c 88	14.2	71.0	817	4	US-09-270-767-18414	Sequence 18414, A
c 89	14.2	71.0	828	4	US-09-489-039A-1281	Sequence 1281, Ap
c 90	14.2	71.0	873	4	US-09-583-110-945	Sequence 945, App
c 91	14.2	71.0	908	4	US-09-976-594-884	Sequence 884, App
c 92	14.2	71.0	1006	4	US-09-610-040-3	Sequence 3, Appl
c 93	14.2	71.0	1006	4	US-09-610-040-9	Sequence 9, Appl
c 94	14.2	71.0	1016	2	US-08-909-965C-2	Sequence 2, Appl
c 95	14.2	71.0	1035	4	US-09-489-039A-1371	Sequence 1371, Ap
c 96	14.2	71.0	1069	4	US-09-270-767-11328	Sequence 11328, A
c 97	14.2	71.0	1176	4	US-09-016-434-1144	Sequence 1144, Ap
c 98	14.2	71.0	1178	3	US-09-091-405-1	Sequence 1, Appl
c 99	14.2	71.0	1479	2	US-08-199-485-1	Sequence 1, Appl
100	14.2	71.0	1569	1	US-08-368-260-1	Sequence 1, Appl

101	14.2	71.0	1569	2	US-08-559-221-1	Sequence 1, Appli	C 174	13.8	69.0	864	4	US-09-248-796A-2143	Sequence 2143, Ap
102	14.2	71.0	1669	3	US-08-860-519-11	Sequence 11, Appl	C 175	13.8	69.0	1012	3	US-08-447-703B-6	Sequence 6, Appli
103	14.2	71.0	1813	4	US-03-270-767-3091	Sequence 3091, Ap	C 176	13.8	69.0	1075	3	US-08-400-006B-6	Sequence 6, Appli
104	14.2	71.0	1813	4	US-03-270-767-18373	Sequence 18373, A	C 177	13.8	69.0	1136	4	US-08-614-221A-2	Sequence 1, Appli
105	14.2	71.0	1860	4	US-03-134-000C-2120	Sequence 2120, Ap	C 178	13.8	69.0	1347	3	US-08-959-749-1	Sequence 1, Appli
106	14.2	71.0	2150	1	US-08-580-680-2	Sequence 2, Appli	C 179	13.8	69.0	1347	3	US-08-351-497-1	Sequence 1, Appli
107	14.2	71.0	2150	1	US-08-480-156A-2	Sequence 2, Appli	C 180	13.8	69.0	1450	4	US-08-956-171E-280	Sequence 280, App
108	14.2	71.0	2150	1	US-08-354-961-2	Sequence 2, Appli	C 181	13.8	69.0	1450	4	US-08-781-986A-280	Sequence 280, App
109	14.2	71.0	2150	2	US-08-581-094-2	Sequence 2, Appli	C 182	13.8	69.0	1458	4	US-09-252-991A-1226	Sequence 1226, Ap
110	14.2	71.0	2150	2	US-08-580-665-2	Sequence 2, Appli	C 183	13.8	69.0	1475	4	US-09-244-805-13	Sequence 13, Appl
111	14.2	71.0	2150	2	US-08-581-142-2	Sequence 2, Appli	C 184	13.8	69.0	1490	4	US-08-865-879-13	Sequence 13, Appl
112	14.2	71.0	2150	3	US-08-581-103-2	Sequence 2, Appli	C 185	13.8	69.0	1635	4	US-09-328-352-3141	Sequence 3141, Ap
113	14.2	71.0	2150	5	PCT-US94-0544A-2	Sequence 2, Appli	C 186	13.8	69.0	1839	4	US-09-270-767-448	Sequence 448, App
114	14.2	71.0	2151	2	US-08-944-449-3	Sequence 3, Appli	C 187	13.8	69.0	1839	4	US-09-270-767-741	Sequence 741, App
115	14.2	71.0	2151	3	US-09-353-362-3	Sequence 3, Appli	C 188	13.8	69.0	1839	4	US-09-270-767-15730	Sequence 15730, A
116	14.2	71.0	2151	4	US-09-023-655-1038	Sequence 1038, Ap	C 189	13.8	69.0	1839	4	US-09-270-767-16023	Sequence 16023, A
117	14.2	71.0	2212	4	US-09-270-767-13857	Sequence 13857, A	C 190	13.8	69.0	2112	4	US-09-252-991A-1294	Sequence 1294, Ap
118	14.2	71.0	2301	3	US-08-085-199B-8	Sequence 8, Appli	C 191	13.8	69.0	2418	4	US-09-270-767-2586	Sequence 2586, Ap
119	14.2	71.0	2403	4	US-09-566-921-94	Sequence 94, Appl	C 192	13.8	69.0	2418	4	US-09-270-767-17868	Sequence 17868, A
120	14.2	71.0	2871	4	US-09-614-221A-506	Sequence 506, Appl	C 193	13.8	69.0	2433	4	US-09-614-221A-293	Sequence 293, App
121	14.2	71.0	2968	4	US-09-270-767-25961	Sequence 25961, A	C 194	13.8	69.0	2558	4	US-09-419-679-1	Sequence 1, Appli
122	14.2	71.0	3061	3	US-09-147-119-6	Sequence 6, Appli	C 195	13.8	69.0	4305	4	US-09-645-593-1	Sequence 1, Appli
123	14.2	71.0	3510	4	US-09-583-110-1748	Sequence 1748, Ap	C 196	13.8	69.0	4338	3	US-09-360-237-4	Sequence 4, Appli
124	14.2	71.0	3606	4	US-09-328-352-1764	Sequence 1764, Ap	C 197	13.8	69.0	4338	3	US-09-891-711-3	Sequence 3, Appli
125	14.2	71.0	3923	2	US-08-139-485-2	Sequence 2, Appli	C 198	13.8	69.0	4576	4	US-08-713-273A-17	Sequence 17, Appl
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127	14.2	71.0	4707	3	US-09-458-791-1	Sequence 1, Appli	C 200	13.8	69.0	5153	5	PCT-US95-04910-8	Sequence 8, Appli
128	14.2	71.0	4707	3	US-09-459-066-1	Sequence 1, Appli	C 201	13.8	69.0	5559	4	US-09-774-528-134	Sequence 134, App
129	14.2	71.0	4707	4	US-09-459-065-1	Sequence 1, Appli	C 202	13.8	69.0	6609	4	US-09-976-594-690	Sequence 690, App
130	14.2	71.0	4768	1	US-07-596-467-1	Sequence 1, Appli	C 203	13.8	69.0	6691	4	US-09-302-681-3	Sequence 3, Appli
131	14.2	71.0	4768	1	US-07-934-374-1	Sequence 1, Appli	C 204	13.8	69.0	6744	3	US-09-037-889-1	Sequence 1, Appli
132	14.2	71.0	4768	1	US-07-783-861C-3	Sequence 3, Appli	C 205	13.8	69.0	6744	4	US-09-038-079-1	Sequence 1, Appli
133	14.2	71.0	5000	3	US-09-104-070-1	Sequence 1, Appli	C 206	13.8	69.0	6855	4	US-09-252-991A-6976	Sequence 6976, Ap
134	14.2	71.0	5176	4	US-09-610-040-6	Sequence 6, Appli	C 207	13.8	69.0	11928	4	US-10-199-024-55	Sequence 55, Appl
135	14.2	71.0	5177	4	US-09-814-915A-79	Sequence 79, Appl	C 208	13.8	69.0	11928	4	US-10-199-024-56	Sequence 56, Appl
136	14.2	71.0	6173	4	US-09-270-767-10540	Sequence 10540, A	C 209	13.8	69.0	11928	4	US-10-199-024-57	Sequence 57, Appl
137	14.2	71.0	9096	3	US-09-147-119-5	Sequence 5, Appli	C 210	13.8	69.0	11928	4	US-10-199-024-58	Sequence 58, Appl
138	14.2	71.0	9370	1	US-08-320-559-27	Sequence 27, Appl	C 211	13.8	69.0	15568	4	US-09-525-906-1	Sequence 1, Appli
139	14.2	71.0	9370	3	US-08-545-860B-27	Sequence 27, Appl	C 212	13.8	69.0	15568	3	US-09-037-889-2	Sequence 2, Appli
140	14.2	71.0	9370	5	PCT-US94-0449E-27	Sequence 27, Appl	C 213	13.8	69.0	16569	3	US-09-377-856-1	Sequence 1, Appli
141	14.2	71.0	12566	4	US-08-961-527-149	Sequence 149, App	C 214	13.8	69.0	16569	4	US-09-302-681-2	Sequence 2, Appli
142	14.2	71.0	15936	3	US-09-147-119-1	Sequence 1, Appli	C 215	13.8	69.0	16569	4	US-09-038-079-2	Sequence 2, Appli
143	14.2	71.0	21338	4	US-08-961-527-20	Sequence 20, Appl	C 216	13.8	69.0	16569	4	US-10-053-611-1	Sequence 1, Appli
144	14.2	71.0	34279	4	US-09-596-002-26	Sequence 26, Appl	C 217	13.8	69.0	22671	3	US-08-976-259-14	Sequence 14, Appl
145	14.2	71.0	55827	4	US-09-813-133A-3	Sequence 3, Appli	C 218	13.8	69.0	22671	4	US-09-956-004-14	Sequence 14, Appl
146	14.2	71.0	118067	4	US-09-497-855A-32	Sequence 32, Appli	C 219	13.8	69.0	41100	4	US-09-755-665-46	Sequence 46, Appl
147	14.2	71.0	1230025	4	US-09-198-452A-1	Sequence 1, Appli	C 220	13.8	69.0	45945	4	US-09-967-669-10	Sequence 10, Appl
148	14.2	70.0	428	4	US-09-621-976-9915	Sequence 9915, Ap	C 221	13.8	69.0	45945	4	US-09-784-316-3	Sequence 3, Appli
149	14.2	70.0	885	3	US-08-924-747-23	Sequence 23, Appl	C 222	13.8	69.0	45945	4	US-10-223-124-3	Sequence 3, Appli
150	14.2	70.0	885	3	US-09-247-373B-23	Sequence 23, Appl	C 223	13.8	69.0	118067	4	US-09-497-855A-32	Sequence 32, Appl
151	14.2	70.0	885	3	US-09-296-715-23	Sequence 23, Appl	C 224	13.8	69.0	786431	4	US-09-751-389-3	Sequence 3, Appli
152	14.2	70.0	897	4	US-09-248-796A-2689	Sequence 2689, App	C 225	13.6	68.0	170	4	US-09-513-999C-34468	Sequence 34468, A
153	14.2	70.0	2169	4	US-08-376-594-315	Sequence 315, App	C 226	13.6	68.0	173	4	US-09-513-999C-19777	Sequence 19777, A
154	14.2	70.0	66884	4	US-09-740-041-3	Sequence 3, Appli	C 227	13.6	68.0	198	4	US-09-270-767-28142	Sequence 28142, A
155	14.2	70.0	1664976	4	US-08-916-421B-1	Sequence 1, Appli	C 228	13.6	68.0	246	4	US-09-513-999C-472	Sequence 472, App
156	14.2	70.0	1664976	4	US-09-692-570-1	Sequence 1, Appli	C 229	13.6	68.0	276	4	US-08-956-171E-1492	Sequence 1492, Ap
157	13.8	69.0	219	4	US-09-543-681A-266	Sequence 266, App	C 230	13.6	68.0	276	4	US-08-781-986A-1492	Sequence 1492, Ap
158	13.8	69.0	278	4	US-09-513-999C-20492	Sequence 20492, A	C 231	13.6	68.0	341	3	US-08-943-731-158	Sequence 158, App
159	13.8	69.0	283	1	US-09-985-799-46	Sequence 46, Appl	C 232	13.6	68.0	341	4	US-09-397-787-259	Sequence 259, App
160	13.8	69.0	283	1	US-08-977-371-46	Sequence 46, Appl	C 233	13.6	68.0	372	4	US-09-513-999C-34169	Sequence 34169, A
161	13.8	69.0	283	1	US-08-594-031-46	Sequence 46, Appl	C 234	13.6	68.0	374	4	US-09-513-999C-13364	Sequence 13364, A
162	13.8	69.0	288	4	US-09-513-999C-32735	Sequence 32735, A	C 235	13.6	68.0	386	4	US-09-621-976-15592	Sequence 15592, A
163	13.8	69.0	291	4	US-09-614-221A-7	Sequence 7, Appli	C 236	13.6	68.0	407	4	US-09-513-999C-24867	Sequence 24867, A
164	13.8	69.0	312	4	US-09-016-434-954	Sequence 954, Appl	C 237	13.6	68.0	417	4	US-09-248-796A-7661	Sequence 7661, Ap
165	13.8	69.0	451	3	US-09-489-868A-11	Sequence 11, Appl	C 238	13.6	68.0	429	4	US-09-854-133-414	Sequence 414, App
166	13.8	69.0	466	3	US-09-489-868A-10	Sequence 10, Appl	C 239	13.6	68.0	459	4	US-09-621-976-2234	Sequence 2234, Ap
167	13.8	69.0	466	4	US-08-621-976-1549	Sequence 1549, App	C 240	13.6	68.0	462	4	US-09-621-976-15424	Sequence 15424, A
168	13.8	69.0	583	4	US-09-621-976-10268	Sequence 10268, A	C 241	13.6	68.0	500	4	US-09-404-879A-17912	Sequence 17912, A
169	13.8	69.0	573	4	US-09-248-796A-2759	Sequence 2759, App	C 242	13.6	68.0	506	4	US-09-338-933-266	Sequence 266, App
170	13.8	69.0	575	4	US-09-270-767-2757	Sequence 2757, App	C 243	13.6	68.0	506	4	US-09-215-681-266	Sequence 266, App
171	13.8	69.0	575	4	US-09-270-767-18039	Sequence 18039, A	C 244	13.6	68.0	506	4	US-09-216-003A-266	Sequence 266, App
172	13.8	69.0	649	4	US-09-976-594-994	Sequence 994, App	C 245	13.6	68.0	506	4	US-09-667-857-266	Sequence 266, App
173	13.8	69.0	852	4	US-09-583-110-1698	Sequence 1698, App	C 246	13.6	68.0	506	4		

C 247	13.6	68.0	507	4	US-09-404-879A-282	Sequence 282, App	320	13.6	68.0	1380	4	US-09-919-0339-304	Sequence 304, App
C 248	13.6	68.0	507	4	US-09-338-933-282	Sequence 282, App	C 321	13.6	68.0	1416	4	US-09-366-009-27	Sequence 27, Appl
C 249	13.6	68.0	507	4	US-09-215-681-282	Sequence 282, App	C 322	13.6	68.0	1416	4	US-08-809-156B-27	Sequence 27, Appl
C 250	13.6	68.0	507	4	US-09-216-003A-282	Sequence 282, App	C 323	13.6	68.0	1445	4	US-09-510-543-10	Sequence 10, Appl
C 251	13.6	68.0	507	4	US-09-667-857-282	Sequence 282, App	C 324	13.6	68.0	1620	6	5449756-10	Patent No. 5449756
C 252	13.6	68.0	507	4	US-09-252-991A-15335	Sequence 15335, A	C 325	13.6	68.0	1683	4	US-09-270-767-10522	Sequence 10522, A
C 253	13.6	68.0	530	4	US-09-270-767-12383	Sequence 12383, A	C 326	13.6	68.0	1702	4	US-09-270-767-10387	Sequence 10387, A
C 254	13.6	68.0	540	4	US-09-513-999C-1397	Sequence 1397, A	C 327	13.6	68.0	1712	2	US-08-632-538-1	Sequence 1, Appl
C 255	13.6	68.0	544	3	US-09-439-133-429	Sequence 429, App	C 328	13.6	68.0	1712	3	US-09-231-240-1	Sequence 1, Appl
C 256	13.6	68.0	544	3	US-09-352-616A-429	Sequence 429, App	C 329	13.6	68.0	1969	1	US-08-106-761-3	Sequence 3, Appl
C 257	13.6	68.0	544	4	US-09-636-215-429	Sequence 429, App	C 330	13.6	68.0	2005	1	US-07-916-901-5	Sequence 5, Appl
C 258	13.6	68.0	544	4	US-09-685-166A-429	Sequence 429, App	C 331	13.6	68.0	2143	3	US-09-097-309-5	Sequence 5, Appl
C 259	13.6	68.0	544	4	US-09-679-426-429	Sequence 429, App	C 332	13.6	68.0	2143	3	US-09-097-171A-9	Sequence 9, Appl
C 260	13.6	68.0	565	4	US-09-270-767-9939	Sequence 9939, Ap	C 333	13.6	68.0	2143	3	US-09-460-587-5	Sequence 5, Appl
C 261	13.6	68.0	573	4	US-09-404-879A-263	Sequence 263, App	C 334	13.6	68.0	2143	4	US-09-940-166A-5	Sequence 5, Appl
C 262	13.6	68.0	573	4	US-09-338-933-263	Sequence 263, App	C 335	13.6	68.0	2288	4	US-09-976-594-1056	Sequence 1056, Ap
C 263	13.6	68.0	573	4	US-09-215-681-263	Sequence 263, App	C 336	13.6	68.0	2306	6	5198359-3	Patent No. 5198359
C 264	13.6	68.0	573	4	US-09-216-003A-263	Sequence 263, App	C 337	13.6	68.0	2306	6	5449756-3	Patent No. 5449756
C 265	13.6	68.0	573	4	US-09-667-857-263	Sequence 263, App	C 338	13.6	68.0	2481	4	US-08-366-009-20	Sequence 20, Appl
C 266	13.6	68.0	605	4	US-09-270-767-27807	Sequence 27807, A	C 339	13.6	68.0	2481	4	US-08-809-156B-20	Sequence 20, Appl
C 267	13.6	68.0	615	4	US-09-799-451-660	Sequence 660, App	C 340	13.6	68.0	2573	4	US-09-620-312D-609	Sequence 609, App
C 268	13.6	68.0	627	2	US-08-993-228-13	Sequence 13, Appl	C 341	13.6	68.0	2613	4	US-09-620-312D-1059	Sequence 1059, Ap
C 269	13.6	68.0	637	4	US-09-270-767-3248	Sequence 3248, Ap	C 342	13.6	68.0	2652	4	US-09-489-039A-4078	Sequence 4078, Ap
C 270	13.6	68.0	637	4	US-09-270-767-18630	Sequence 18630, A	C 343	13.6	68.0	2731	4	US-09-976-594-281	Sequence 281, App
C 271	13.6	68.0	699	4	US-09-107-532A-1581	Sequence 1581, Ap	C 344	13.6	68.0	2829	4	US-10-004-542-1	Sequence 1, Appl
C 272	13.6	68.0	708	3	US-08-998-416-997	Sequence 997, App	C 345	13.6	68.0	2829	4	US-10-430-787-1	Sequence 1, Appl
C 273	13.6	68.0	715	4	US-09-270-767-12098	Sequence 12098, A	C 346	13.6	68.0	3074	4	US-09-976-594-1012	Sequence 1012, Ap
C 274	13.6	68.0	715	4	US-09-270-767-13236	Sequence 13236, A	C 347	13.6	68.0	3074	4	US-09-919-039-380	Sequence 380, App
C 275	13.6	68.0	720	4	US-09-404-879A-239	Sequence 239, App	C 348	13.6	68.0	3095	1	US-08-119-773-1	Sequence 1, Appl
C 276	13.6	68.0	720	4	US-09-338-933-239	Sequence 239, App	C 349	13.6	68.0	3095	4	US-09-614-915A-9	Sequence 9, Appl
C 277	13.6	68.0	720	4	US-09-215-681-239	Sequence 239, App	C 350	13.6	68.0	3136	4	US-09-751-389-1	Sequence 1, Appl
C 278	13.6	68.0	720	4	US-09-216-003A-239	Sequence 239, App	C 351	13.6	68.0	3220	4	US-10-004-542-5	Sequence 5, Appl
C 279	13.6	68.0	720	4	US-09-667-857-239	Sequence 239, App	C 352	13.6	68.0	3220	4	US-10-430-787-5	Sequence 5, Appl
C 280	13.6	68.0	721	3	US-08-998-416-803	Sequence 803, App	C 353	13.6	68.0	3246	4	US-09-614-221A-228	Sequence 228, App
C 281	13.6	68.0	750	4	US-09-583-110-1454	Sequence 1454, Ap	C 354	13.6	68.0	3258	4	US-09-799-451-586	Sequence 586, App
C 282	13.6	68.0	776	4	US-09-404-879A-234	Sequence 234, App	C 355	13.6	68.0	3268	4	US-09-566-921-91	Sequence 91, Appl
C 283	13.6	68.0	776	4	US-09-338-933-234	Sequence 234, App	C 356	13.6	68.0	3429	3	US-08-097-997A-10	Sequence 10, Appl
C 284	13.6	68.0	776	4	US-09-215-681-234	Sequence 234, App	C 357	13.6	68.0	3429	3	US-08-665-574C-10	Sequence 10, Appl
C 285	13.6	68.0	776	4	US-09-216-003A-234	Sequence 234, App	C 358	13.6	68.0	3429	3	US-08-945-994-10	Sequence 10, Appl
C 286	13.6	68.0	776	4	US-09-667-857-234	Sequence 234, App	C 359	13.6	68.0	3538	4	US-09-963-137-201	Sequence 201, App
C 287	13.6	68.0	789	4	US-09-107-532A-471	Sequence 471, App	C 360	13.6	68.0	3541	4	US-09-963-137-160	Sequence 160, App
C 288	13.6	68.0	805	4	US-09-404-879A-235	Sequence 235, App	C 361	13.6	68.0	3541	4	US-09-023-655-1205	Sequence 1205, Ap
C 289	13.6	68.0	805	4	US-09-338-933-235	Sequence 235, App	C 362	13.6	68.0	3592	2	US-08-469-537A-100	Sequence 100, App
C 290	13.6	68.0	805	4	US-09-215-681-235	Sequence 235, App	C 363	13.6	68.0	3969	1	US-08-241-853-1	Sequence 1, Appl
C 291	13.6	68.0	805	4	US-09-216-003A-235	Sequence 235, App	C 364	13.6	68.0	3969	2	US-08-850-917-1	Sequence 1, Appl
C 292	13.6	68.0	805	4	US-09-667-857-235	Sequence 235, App	C 365	13.6	68.0	4027	2	US-08-551-356-5	Sequence 5, Appl
C 293	13.6	68.0	808	4	US-09-404-879A-241	Sequence 241, App	C 366	13.6	68.0	4027	5	PCI-US93-12887-5	Sequence 5, Appl
C 294	13.6	68.0	808	4	US-09-338-933-241	Sequence 241, App	C 367	13.6	68.0	4082	4	US-08-956-171E-261	Sequence 261, App
C 295	13.6	68.0	808	4	US-09-215-681-241	Sequence 241, App	C 368	13.6	68.0	4082	4	US-08-781-986A-261	Sequence 261, App
C 296	13.6	68.0	808	4	US-09-216-003A-241	Sequence 241, App	C 369	13.6	68.0	4234	1	US-08-446-038B-1	Sequence 1, Appl
C 297	13.6	68.0	808	4	US-09-667-857-241	Sequence 241, App	C 370	13.6	68.0	4234	1	US-08-446-010B-1	Sequence 1, Appl
C 298	13.6	68.0	808	4	US-09-509-347-6	Sequence 6, Appl	C 371	13.6	68.0	4234	1	US-08-805-445-1	Sequence 1, Appl
C 299	13.6	68.0	927	3	US-09-027-449-59	Sequence 59, Appl	C 372	13.6	68.0	4234	2	US-08-064-087D-1	Sequence 1, Appl
C 300	13.6	68.0	927	3	US-08-804-444A-59	Sequence 59, Appl	C 373	13.6	68.0	4234	2	US-09-066-208-1	Sequence 1, Appl
C 301	13.6	68.0	927	3	US-09-036-985-59	Sequence 59, Appl	C 374	13.6	68.0	4460	4	US-09-814-915A-10	Sequence 10, Appl
C 302	13.6	68.0	927	4	US-09-121-952A-59	Sequence 59, Appl	C 375	13.6	68.0	4460	3	US-09-453-702B-21	Sequence 21, Appl
C 303	13.6	68.0	927	4	US-09-234-340A-59	Sequence 59, Appl	C 376	13.6	68.0	5467	2	US-08-605-106-7	Sequence 7, Appl
C 304	13.6	68.0	1017	3	US-08-913-842-14	Sequence 14, Appl	C 377	13.6	68.0	6550	3	US-09-422-712B-1	Sequence 1, Appl
C 305	13.6	68.0	1042	3	US-09-216-003A-77	Sequence 77, Appl	C 378	13.6	68.0	6550	3	US-09-607-756-1	Sequence 1, Appl
C 306	13.6	68.0	1042	3	US-08-846-762-98	Sequence 98, Appl	C 379	13.6	68.0	6563	3	US-09-027-449-61	Sequence 61, Appl
C 307	13.6	68.0	1059	4	US-09-252-991A-12152	Sequence 12152, A	C 380	13.6	68.0	6563	3	US-08-804-444A-61	Sequence 61, Appl
C 308	13.6	68.0	1074	4	US-09-270-767-25777	Sequence 25777, A	C 381	13.6	68.0	6563	3	US-09-026-985-61	Sequence 61, Appl
C 309	13.6	68.0	1127	3	US-08-913-842-5	Sequence 5, Appl	C 382	13.6	68.0	6563	4	US-09-121-952A-61	Sequence 61, Appl
C 310	13.6	68.0	1166	1	US-08-121-063-7	Sequence 7, Appl	C 383	13.6	68.0	6563	4	US-09-234-340A-61	Sequence 61, Appl
C 311	13.6	68.0	1179	4	US-08-489-039A-1542	Sequence 1542, Ap	C 384	13.6	68.0	6703	4	US-09-331-403-1	Sequence 1, Appl
C 312	13.6	68.0	1185	4	US-09-270-767-25940	Sequence 25940, A	C 385	13.6	68.0	7679	4	US-09-220-132-38	Sequence 38, Appl
C 313	13.6	68.0	1227	4	US-09-328-352-2381	Sequence 2381, A	C 386	13.6	68.0	7680	4	US-09-023-655-1289	Sequence 1289, Ap
C 314	13.6	68.0	1263	4	US-09-336-536-8	Sequence 8, Appl	C 387	13.6	68.0	7680	5	PCI-US95-09819-6	Sequence 6, Appl
C 315	13.6	68.0	1263	4	US-09-252-991A-15423	Sequence 15423, A	C 388	13.6	68.0	7705	1	US-08-259-569-16	Sequence 16, Appl
C 316	13.6	68.0	1305	4	US-09-252-991A-15257	Sequence 15257, A	C 389	13.6	68.0	7705	2	US-08-826-885-16	Sequence 16, Appl
C 317	13.6	68.0	1359	4	US-09-614-221A-448	Sequence 448, App	C 390	13.6	68.0	7705	6	5455158-2	Patent No. 5455158
C 318	13.6	68.0	1374	4	US-09-366-009-26	Sequence 26, Appl	C 391	13.6	68.0	7803	2	US-08-551-356-1	Sequence 1, Appl
C 319	13.6	68.0	1374	4	US-08-809-156B-26	Sequence 26, Appl	C 392	13.6	68.0	7803	5	PCI-US93-12687-1	Sequence 1, Appl

C 393	13.6	68.0	8044	4	US-09-566-921-135	Sequence 135, Appl	466	13.2	66.0	239	3	US-09-247-155-84	Sequence 84, Appl
C 394	13.6	68.0	8378	5	PCT-US91-09055-1	Sequence 1, Appl	467	13.2	66.0	249	4	US-09-134-000C-2099	Sequence 2099, Ap
C 395	13.6	68.0	9578	4	US-08-961-527-127	Sequence 127, Appl	C 468	13.2	66.0	250	3	US-08-944-483-4	Sequence 4, Appl
C 396	13.6	68.0	15225	2	US-08-892-403A-2	Sequence 2, Appl	C 469	13.2	66.0	259	4	US-09-513-999C-25332	Sequence 25332, A
C 397	13.6	68.0	15225	4	US-09-291-894-2	Sequence 2, Appl	C 470	13.2	66.0	267	4	US-09-313-294A-4595	Sequence 4595, Ap
C 398	13.6	68.0	17606	3	US-08-943-731-4	Sequence 4, Appl	471	13.2	66.0	269	4	US-09-513-999C-21588	Sequence 21588, A
C 399	13.6	68.0	17606	3	US-08-850-880-11	Sequence 11, Appl	472	13.2	66.0	305	4	US-09-513-999C-34437	Sequence 34437, A
C 400	13.6	68.0	19182	2	US-08-944-916-11	Sequence 11, Appl	473	13.2	66.0	312	4	US-09-489-039A-4168	Sequence 4168, Ap
C 401	13.6	68.0	19182	4	US-09-272-432A-11	Sequence 11, Appl	474	13.2	66.0	342	4	US-09-107-532A-742	Sequence 742, App
C 402	13.6	68.0	24417	2	US-08-846-762-1	Sequence 1, Appl	475	13.2	66.0	357	3	US-08-905-223-251	Sequence 251, App
C 403	13.6	68.0	36741	3	US-09-301-665-3	Sequence 3, Appl	476	13.2	66.0	377	4	US-09-513-999C-33042	Sequence 33042, A
C 404	13.6	68.0	45716	3	US-08-965-048-5	Sequence 5, Appl	477	13.2	66.0	400	2	US-08-651-163-1	Sequence 1, Appl
C 405	13.6	68.0	45989	3	US-08-985-048-5	Sequence 6, Appl	C 478	13.2	66.0	420	4	US-09-583-110-570	Sequence 570, App
C 406	13.6	68.0	45989	1	US-08-471-119A-1	Sequence 1, Appl	C 479	13.2	66.0	421	4	US-09-621-976-12538	Sequence 12538, A
C 407	13.6	68.0	70559	4	US-09-409-800B-1	Sequence 1, Appl	480	13.2	66.0	438	4	US-09-513-999C-205	Sequence 205, App
C 408	13.6	68.0	152331	3	US-09-128-155-16	Sequence 16, Appl	C 481	13.2	66.0	452	4	US-09-621-976-1341	Sequence 1341, Ap
C 409	13.6	68.0	1830121	4	US-09-557-884-1	Sequence 1, Appl	482	13.2	66.0	456	3	US-09-040-984-79	Sequence 79, Appl
C 410	13.6	68.0	1830121	4	US-09-643-990A-1	Sequence 1, Appl	483	13.2	66.0	456	3	US-09-123-912-79	Sequence 79, Appl
C 411	13.6	68.0	1830121	4	US-10-329-960-1	Sequence 1, Appl	484	13.2	66.0	456	4	US-09-643-597-79	Sequence 79, Appl
C 412	13.4	67.0	21	3	US-08-282-694A-44	Sequence 44, Appl	485	13.2	66.0	456	4	US-09-480-884A-79	Sequence 79, Appl
C 413	13.4	67.0	392	4	US-08-513-999C-952	Sequence 952, Appl	486	13.2	66.0	456	4	US-09-542-615A-79	Sequence 79, Appl
C 414	13.4	67.0	399	4	US-08-513-999C-27214	Sequence 27214, A	487	13.2	66.0	456	4	US-09-608-421B-79	Sequence 79, Appl
C 415	13.4	67.0	466	4	US-09-621-976-13422	Sequence 13422, A	488	13.2	66.0	456	4	US-09-221-107-79	Sequence 79, Appl
C 416	13.4	67.0	543	4	US-09-489-039A-5453	Sequence 5453, Ap	489	13.2	66.0	456	4	US-09-466-396A-79	Sequence 79, Appl
C 417	13.4	67.0	633	4	US-09-489-039A-1300	Sequence 1300, Ap	490	13.2	66.0	456	4	US-09-476-496A-79	Sequence 79, Appl
C 418	13.4	67.0	733	4	US-09-470-276-61	Sequence 61, Appl	491	13.2	66.0	456	4	US-09-630-940B-79	Sequence 79, Appl
C 419	13.4	67.0	1128	3	US-08-795-473B-1	Sequence 1, Appl	C 492	13.2	66.0	465	4	US-09-621-976-12532	Sequence 12532, A
C 420	13.4	67.0	1128	4	US-09-439-856-1	Sequence 1, Appl	493	13.2	66.0	477	4	US-09-513-999C-26144	Sequence 26144, A
C 421	13.4	67.0	1145	6	5510472-1	Patent No. 5510472	C 494	13.2	66.0	483	4	US-09-543-681A-196	Sequence 196, App
C 422	13.4	67.0	1227	4	US-09-248-796A-488	Sequence 488, App	C 495	13.2	66.0	488	4	US-09-621-976-12546	Sequence 12546, A
C 423	13.4	67.0	1257	4	US-09-543-681A-3640	Sequence 3640, Ap	C 496	13.2	66.0	506	4	US-09-621-976-15483	Sequence 15483, A
C 424	13.4	67.0	1556	2	US-08-861-857-1	Sequence 1, Appl	C 497	13.2	66.0	517	4	US-09-270-776-27960	Sequence 27960, A
C 425	13.4	67.0	1556	3	US-09-233-342A-1	Sequence 1, Appl	C 498	13.2	66.0	525	3	US-09-280-116-154	Sequence 154, App
C 426	13.4	67.0	1572	4	US-09-540-236-679	Sequence 679, App	C 499	13.2	66.0	526	4	US-09-857-556A-13	Sequence 13, Appl
C 427	13.4	67.0	1824	4	US-09-620-312D-811	Sequence 811, App	C 500	13.2	66.0	536	4	US-09-436-698C-7	Sequence 7, Appl
C 428	13.4	67.0	1983	4	US-08-583-110-1315	Sequence 1315, Ap	C 501	13.2	66.0	546	4	US-09-513-999C-1051	Sequence 1051, Ap
C 429	13.4	67.0	2019	2	US-08-245-511-46	Sequence 46, Appl	502	13.2	66.0	550	4	US-09-404-879A-264	Sequence 264, App
C 430	13.4	67.0	2019	2	US-08-600-993A-46	Sequence 46, Appl	503	13.2	66.0	550	4	US-09-338-933-264	Sequence 264, App
C 431	13.4	67.0	2073	4	US-09-614-221A-242	Sequence 242, App	504	13.2	66.0	550	4	US-09-215-681-264	Sequence 264, App
C 432	13.4	67.0	2300	4	US-09-591-095-1	Sequence 1, Appl	505	13.2	66.0	550	4	US-09-216-003A-264	Sequence 264, App
C 433	13.4	67.0	2342	4	US-09-904-615-12	Sequence 12, Appl	506	13.2	66.0	550	4	US-09-667-857-264	Sequence 264, App
C 434	13.4	67.0	2399	2	US-08-968-106-9	Sequence 9, Appl	C 507	13.2	66.0	564	4	US-09-513-999C-1047	Sequence 1047, Ap
C 435	13.4	67.0	2399	4	US-09-338-125-9	Sequence 9, Appl	C 508	13.2	66.0	566	4	US-09-513-999C-1052	Sequence 1052, Ap
C 436	13.4	67.0	2785	4	US-09-774-528-105	Sequence 105, App	509	13.2	66.0	567	3	US-09-385-982-425	Sequence 425, App
C 437	13.4	67.0	4047	3	US-09-534-407-4	Sequence 4, Appl	C 510	13.2	66.0	568	4	US-09-702-705-171	Sequence 171, App
C 438	13.4	67.0	4047	4	US-09-999-201B-3	Sequence 3, Appl	C 511	13.2	66.0	568	4	US-09-736-457-171	Sequence 171, App
C 439	13.4	67.0	4047	4	US-10-281-673A-3	Sequence 3, Appl	C 512	13.2	66.0	568	4	US-09-614-124B-171	Sequence 171, App
C 440	13.4	67.0	5658	3	US-08-981-450A-23	Sequence 23, Appl	C 513	13.2	66.0	568	4	US-09-671-325-171	Sequence 171, App
C 441	13.4	67.0	10711	4	US-08-961-527-145	Sequence 145, App	C 514	13.2	66.0	568	4	US-09-589-184-171	Sequence 171, App
C 442	13.4	67.0	20165	4	US-09-609-816-7	Sequence 17, Appl	C 515	13.2	66.0	580	4	US-09-688-824-171	Sequence 171, App
C 443	13.4	67.0	40090	4	US-09-820-004-3	Sequence 3, Appl	C 516	13.2	66.0	580	4	US-09-513-999C-1049	Sequence 1049, Ap
C 444	13.4	67.0	48974	3	US-09-920-422-17	Sequence 17, Appl	C 517	13.2	66.0	595	4	US-09-513-999C-1046	Sequence 1046, Ap
C 445	13.4	67.0	72928	3	US-09-099-913-1	Sequence 1, Appl	C 518	13.2	66.0	623	3	US-09-385-982-207	Sequence 207, App
C 446	13.4	67.0	90050	4	US-09-245-041-5	Sequence 5, Appl	C 519	13.2	66.0	696	4	US-09-248-796A-13483	Sequence 13483, A
C 447	13.4	67.0	90050	4	US-09-358-055B-5	Sequence 5, Appl	C 520	13.2	66.0	826	4	US-09-621-976-3172	Sequence 3172, Ap
C 448	13.4	67.0	90050	4	US-09-833-238-5	Sequence 5, Appl	C 521	13.2	66.0	833	2	US-08-790-137-2	Sequence 2, Appl
C 449	13.4	67.0	96109	4	US-09-596-002-35	Sequence 35, Appl	C 522	13.2	66.0	876	4	US-09-602-787A-187	Sequence 187, App
C 450	13.2	66.0	37	4	US-09-549-848B-56	Sequence 56, Appl	C 523	13.2	66.0	893	4	US-09-513-999C-14942	Sequence 14942, A
C 451	13.2	66.0	47	4	US-09-422-978-1597	Sequence 1597, Ap	524	13.2	66.0	897	4	US-09-556-877-120	Sequence 120, App
C 452	13.2	66.0	112	4	US-09-270-767-4317	Sequence 4317, Ap	525	13.2	66.0	897	4	US-09-556-877-130	Sequence 130, App
C 453	13.2	66.0	112	4	US-09-270-767-19559	Sequence 19559, A	526	13.2	66.0	897	4	US-09-556-877-132	Sequence 132, App
C 454	13.2	66.0	198	4	US-09-621-976-13616	Sequence 13616, A	527	13.2	66.0	897	4	US-09-620-412C-120	Sequence 120, App
C 455	13.2	66.0	209	2	US-08-682-787-20	Sequence 20, Appl	528	13.2	66.0	897	4	US-09-620-412C-130	Sequence 130, App
C 456	13.2	66.0	209	3	US-09-097-199-20	Sequence 20, Appl	529	13.2	66.0	897	4	US-08-620-412C-132	Sequence 132, App
C 457	13.2	66.0	215	4	US-09-313-294A-6915	Sequence 6915, Ap	530	13.2	66.0	897	4	US-09-598-419-120	Sequence 120, App
C 458	13.2	66.0	234	4	US-08-469-260A-30	Sequence 30, Appl	531	13.2	66.0	897	4	US-09-598-419-130	Sequence 130, App
C 459	13.2	66.0	234	4	US-08-469-260A-391	Sequence 391, App	532	13.2	66.0	897	4	US-09-598-419-132	Sequence 132, App
C 460	13.2	66.0	234	4	US-08-488-446-30	Sequence 30, Appl	C 533	13.2	66.0	911	4	US-09-513-999C-14938	Sequence 14938, A
C 461	13.2	66.0	234	4	US-08-488-446-391	Sequence 391, App	C 534	13.2	66.0	912	4	US-09-328-352-3591	Sequence 3591, Ap
C 462	13.2	66.0	234	4	US-08-467-344A-30	Sequence 30, Appl	C 535	13.2	66.0	913	4	US-09-513-999C-14937	Sequence 14937, A
C 463	13.2	66.0	234	4	US-08-467-344A-391	Sequence 391, App	C 536	13.2	66.0	927	4	US-09-513-999C-14936	Sequence 14936, A
C 464	13.2	66.0	234	4	US-08-424-550B-30	Sequence 30, Appl	C 537	13.2	66.0	942	4	US-09-513-999C-3890	Sequence 3890, Ap
C 465	13.2	66.0	234	4	US-08-424-550B-391	Sequence 391, App	538	13.2	66.0	948	4	US-09-543-681A-3947	Sequence 3947, Ap



539	13.2	66.0	999	3	US-09-134-001C-2392	Sequence 2392, Ap	612	13.2	66.0	2735	2	US-08-494-440B-11	Sequence 11, Appl
540	13.2	66.0	1026	4	US-09-394-110A-3	Sequence 3, Appl	613	13.2	66.0	2735	2	US-08-533-901B-11	Sequence 11, Appl
541	13.2	66.0	1035	4	US-09-248-796A-1418	Sequence 1418, Ap	614	13.2	66.0	2735	2	US-08-839-032A-11	Sequence 11, Appl
542	13.2	66.0	1052	4	US-09-386-642-10	Sequence 10, Appl	615	13.2	66.0	2735	2	US-08-839-031A-11	Sequence 11, Appl
543	13.2	66.0	1059	4	US-09-328-352-2355	Sequence 2355, Ap	616	13.2	66.0	2735	3	US-09-185-258C-11	Sequence 11, Appl
544	13.2	66.0	1076	4	US-08-956-171E-41	Sequence 41, Appl	617	13.2	66.0	2735	5	PCT-US95-12724-11	Sequence 11, Appl
545	13.2	66.0	1076	4	US-08-781-986A-41	Sequence 41, Appl	618	13.2	66.0	2809	4	US-09-620-312D-171	Sequence 171, App
546	13.2	66.0	1114	3	US-08-468-413-1	Sequence 1, Appl	619	13.2	66.0	2820	1	US-08-162-809-5	Sequence 5, Appl
547	13.2	66.0	1114	3	US-08-162-508-1	Sequence 1, Appl	620	13.2	66.0	2840	5	PCT-US93-06251-64	Sequence 64, Appl
548	13.2	66.0	1114	5	PCT-US95-07169-1	Sequence 1, Appl	621	13.2	66.0	2869	1	US-08-369-796-11	Sequence 11, Appl
549	13.2	66.0	1137	4	US-09-583-110-1744	Sequence 1744, Ap	622	13.2	66.0	2869	2	US-08-852-081-11	Sequence 11, Appl
550	13.2	66.0	1146	4	US-09-205-258-247	Sequence 247, App	623	13.2	66.0	2869	2	US-08-820-754-11	Sequence 11, Appl
551	13.2	66.0	1166	3	US-08-944-483-7	Sequence 7, Appl	624	13.2	66.0	2869	3	US-08-956-652-11	Sequence 11, Appl
552	13.2	66.0	1192	3	US-08-944-483-8	Sequence 8, Appl	625	13.2	66.0	2869	3	US-08-956-652-11	Sequence 11, Appl
553	13.2	66.0	1204	4	US-10-140-002-505	Sequence 505, App	626	13.2	66.0	2869	3	US-08-948-547-11	Sequence 11, Appl
554	13.2	66.0	1236	3	US-09-445-472-2	Sequence 2, Appl	627	13.2	66.0	2869	3	US-09-288-461-82	Sequence 82, Appl
555	13.2	66.0	1236	4	US-10-090-524-2	Sequence 2, Appl	628	13.2	66.0	2869	3	US-09-364-970-9	Sequence 9, Appl
556	13.2	66.0	1279	2	US-08-872-719-1	Sequence 1, Appl	629	13.2	66.0	2869	3	US-08-956-653A-11	Sequence 11, Appl
557	13.2	66.0	1279	3	US-08-957-302A-11	Sequence 11, Appl	630	13.2	66.0	2869	4	US-08-212-185-11	Sequence 11, Appl
558	13.2	66.0	1279	3	US-09-336-890-1	Sequence 1, Appl	631	13.2	66.0	2869	4	US-09-758-881-82	Sequence 82, Appl
559	13.2	66.0	1279	3	US-09-542-403-11	Sequence 11, Appl	632	13.2	66.0	2869	5	PCT-US95-17025-11	Sequence 11, Appl
560	13.2	66.0	1279	4	US-09-668-499-1	Sequence 1, Appl	633	13.2	66.0	2873	3	US-08-630-915A-193	Sequence 193, App
561	13.2	66.0	1292	4	US-09-205-258-189	Sequence 189, App	634	13.2	66.0	2873	4	US-09-879-957-193	Sequence 193, App
562	13.2	66.0	1314	3	US-08-025-059-2	Sequence 2, Appl	635	13.2	66.0	2875	5	PCT-US93-06251-63	Sequence 63, Appl
563	13.2	66.0	1359	4	US-08-799-451-677	Sequence 677, App	636	13.2	66.0	3001	4	US-09-539-333D-179	Sequence 179, App
564	13.2	66.0	1395	4	US-08-957-302A-3	Sequence 3, Appl	637	13.2	66.0	3026	4	US-09-149-476-317	Sequence 317, App
565	13.2	66.0	1395	3	US-09-542-403-3	Sequence 3, Appl	638	13.2	66.0	3054	4	US-09-149-476-194	Sequence 194, App
566	13.2	66.0	1395	3	US-09-711-164-259	Sequence 259, App	639	13.2	66.0	3116	2	US-08-449-645A-14	Sequence 14, Appl
567	13.2	66.0	1402	4	US-09-976-594-937	Sequence 937, App	640	13.2	66.0	3116	2	US-08-702-367A-14	Sequence 14, Appl
568	13.2	66.0	1493	4	US-09-482-373-17	Sequence 17, Appl	641	13.2	66.0	3116	5	PCT-US95-04681-14	Sequence 14, Appl
569	13.2	66.0	1509	4	US-09-134-000C-1543	Sequence 1543, Ap	642	13.2	66.0	3118	4	US-09-710-279-4206	Sequence 4206, Ap
570	13.2	66.0	1566	3	US-08-894-818B-4	Sequence 4, Appl	643	13.2	66.0	3162	2	US-08-449-645A-12	Sequence 12, Appl
571	13.2	66.0	1575	3	US-08-957-302A-1	Sequence 1, Appl	644	13.2	66.0	3162	2	US-08-702-367A-12	Sequence 12, Appl
572	13.2	66.0	1575	3	US-09-542-403-1	Sequence 1, Appl	645	13.2	66.0	3162	5	PCT-US95-04681-12	Sequence 12, Appl
573	13.2	66.0	1674	4	US-09-482-373-78	Sequence 78, Appl	646	13.2	66.0	3195	4	US-09-254-594-1	Sequence 1, Appl
574	13.2	66.0	1685	1	US-07-708-038-1	Sequence 1, Appl	647	13.2	66.0	3304	4	US-09-919-172-63	Sequence 63, Appl
575	13.2	66.0	1685	1	US-08-127-995-1	Sequence 1, Appl	648	13.2	66.0	3348	1	US-08-222-616-34	Sequence 34, Appl
576	13.2	66.0	1747	1	US-08-620-312D-1062	Sequence 1062, Ap	649	13.2	66.0	3348	3	US-08-448-648-34	Sequence 34, Appl
577	13.2	66.0	1751	4	US-09-673-300-1	Sequence 1, Appl	650	13.2	66.0	3348	4	US-09-982-610-34	Sequence 34, Appl
578	13.2	66.0	1796	4	US-09-270-767-30632	Sequence 30632, A	651	13.2	66.0	3348	5	PCT-US95-04228-34	Sequence 34, Appl
579	13.2	66.0	1906	4	US-09-023-655-1354	Sequence 5, Appl	652	13.2	66.0	3493	3	US-09-710-279-4206	Sequence 4206, Ap
580	13.2	66.0	1941	5	PCT-US91-07635-5	Sequence 5, Appl	653	13.2	66.0	3515	3	US-09-453-702B-54	Sequence 54, Appl
581	13.2	66.0	1962	3	US-08-894-818B-34	Sequence 34, Appl	654	13.2	66.0	3597	3	US-09-095-758-4	Sequence 4, Appl
582	13.2	66.0	1962	3	US-09-445-472-15	Sequence 15, Appl	655	13.2	66.0	3597	3	US-09-422-968-4	Sequence 4, Appl
583	13.2	66.0	1962	3	US-10-090-624-15	Sequence 15, Appl	656	13.2	66.0	3597	4	US-09-708-015A-4	Sequence 4, Appl
584	13.2	66.0	2031	4	US-09-543-681A-1771	Sequence 1771, Ap	657	13.2	66.0	3606	4	US-08-956-171E-43	Sequence 43, Appl
585	13.2	66.0	2097	4	US-09-620-312D-17	Sequence 17, Appl	658	13.2	66.0	3606	4	US-08-781-986A-43	Sequence 43, Appl
586	13.2	66.0	2158	1	US-08-698-551-1	Sequence 1, Appl	659	13.2	66.0	3663	4	US-09-919-172-84	Sequence 84, Appl
587	13.2	66.0	2158	2	US-08-602-328-1	Sequence 1, Appl	660	13.2	66.0	3906	2	US-08-469-537A-102	Sequence 102, App
588	13.2	66.0	2158	2	US-08-649-341A-1	Sequence 1, Appl	661	13.2	66.0	3935	4	US-09-060-482-1	Sequence 1, Appl
589	13.2	66.0	2158	2	US-08-434-440B-1	Sequence 1, Appl	662	13.2	66.0	4041	1	US-08-147-812-4	Sequence 4, Appl
590	13.2	66.0	2158	2	US-08-533-901B-1	Sequence 1, Appl	663	13.2	66.0	4110	3	US-09-123-708-1	Sequence 1, Appl
591	13.2	66.0	2158	2	US-08-839-032A-1	Sequence 1, Appl	664	13.2	66.0	4110	3	US-09-123-708-1	Sequence 1, Appl
592	13.2	66.0	2158	2	US-08-839-031A-1	Sequence 1, Appl	665	13.2	66.0	4165	1	US-08-442-248-1	Sequence 1, Appl
593	13.2	66.0	2158	3	US-09-185-258C-1	Sequence 1, Appl	666	13.2	66.0	4165	1	US-08-147-812-6	Sequence 6, Appl
594	13.2	66.0	2158	5	PCT-US95-12724-1	Sequence 1, Appl	667	13.2	66.0	4165	1	US-08-440-815-1	Sequence 1, Appl
595	13.2	66.0	2295	4	US-09-270-767-12223	Sequence 12223, A	668	13.2	66.0	4165	3	US-08-486-449-1	Sequence 1, Appl
596	13.2	66.0	2300	3	US-09-471-016-13	Sequence 13, Appl	669	13.2	66.0	4165	3	US-08-578-684-1	Sequence 1, Appl
597	13.2	66.0	2300	4	US-09-591-095-1	Sequence 1, Appl	670	13.2	66.0	4268	4	US-08-469-260A-80	Sequence 80, Appl
598	13.2	66.0	2310	1	US-08-416-581B-6	Sequence 6, Appl	671	13.2	66.0	4268	4	US-08-468-448-80	Sequence 80, Appl
599	13.2	66.0	2351	4	US-09-270-767-14459	Sequence 14459, A	672	13.2	66.0	4268	4	US-08-467-344A-80	Sequence 80, Appl
600	13.2	66.0	2430	4	US-09-620-312D-176	Sequence 176, Appl	673	13.2	66.0	4268	4	US-08-424-550B-80	Sequence 80, Appl
601	13.2	66.0	2446	3	US-09-310-463-11	Sequence 11, Appl	674	13.2	66.0	4618	4	US-09-620-312D-150	Sequence 150, App
602	13.2	66.0	2446	4	US-08-842-248A-11	Sequence 11, Appl	675	13.2	66.0	5129	4	US-09-976-594-964	Sequence 964, App
603	13.2	66.0	2559	2	US-08-866-152-4	Sequence 4, Appl	676	13.2	66.0	5262	4	US-09-248-796A-5051	Sequence 5051, Ap
604	13.2	66.0	2559	3	US-09-196-222-4	Sequence 4, Appl	677	13.2	66.0	5475	4	US-09-543-681A-837	Sequence 837, App
605	13.2	66.0	2591	4	US-09-023-655-1000	Sequence 1000, Ap	678	13.2	66.0	5894	3	US-08-665-259-24	Sequence 24, Appl
606	13.2	66.0	2652	1	US-08-416-581B-7	Sequence 7, Appl	679	13.2	66.0	5894	3	US-08-763-500-24	Sequence 24, Appl
607	13.2	66.0	2652	1	US-08-416-581B-8	Sequence 8, Appl	680	13.2	66.0	6002	2	US-08-698-551-15	Sequence 15, Appl
608	13.2	66.0	2701	4	US-09-839-709-1	Sequence 1, Appl	681	13.2	66.0	6002	2	US-08-602-228-15	Sequence 15, Appl
609	13.2	66.0	2718	4	US-09-248-796A-1603	Sequence 1603, Ap	682	13.2	66.0	6002	2	US-08-839-032A-15	Sequence 15, Appl
610	13.2	66.0	2735	1	US-08-698-551-11	Sequence 11, Appl	683	13.2	66.0	6002	2	US-09-185-258C-15	Sequence 15, Appl
611	13.2	66.0	2735	2	US-08-602-228-11	Sequence 11, Appl	684	13.2	66.0	6151	4	US-09-799-451-528	Sequence 528, App

685	13.2	66.0	6223	4	US-09-620-312D-459	Sequence 459, App	C 758	12.8	64.0	213	4	US-09-328-352-352	Sequence 952, App
686	13.2	66.0	6304	4	US-09-620-312D-461	Sequence 461, App	759	12.8	64.0	257	4	US-09-600-319-1	Sequence 1, Appli
687	13.2	66.0	6382	4	US-09-620-312D-460	Sequence 460, App	760	12.8	64.0	270	4	US-09-313-294A-1723	Sequence 1723, Ap
c 688	13.2	66.0	6525	3	US-08-762-500-74	Sequence 74, Appl	761	12.8	64.0	285	4	US-09-513-999C-29457	Sequence 29457, A
689	13.2	66.0	6617	4	US-09-976-594-268	Sequence 268, App	762	12.8	64.0	290	4	US-09-513-999C-34933	Sequence 34933, A
690	13.2	66.0	7063	4	US-09-485-632B-5	Sequence 5, Appli	763	12.8	64.0	294	4	US-09-328-352-3519	Sequence 3519, Ap
691	13.2	66.0	7543	4	US-09-774-528-163	Sequence 163, App	764	12.8	64.0	299	4	US-09-621-976-16226	Sequence 16226, A
692	13.2	66.0	7812	4	US-09-485-632B-9	Sequence 9, Appli	765	12.8	64.0	300	4	US-09-621-976-16227	Sequence 16227, A
c 693	13.2	66.0	8442	3	US-09-272-032-6	Sequence 6, Appli	766	12.8	64.0	351	4	US-09-489-039A-4451	Sequence 4451, Ap
694	13.2	66.0	8912	4	US-08-469-260A-11	Sequence 11, Appl	767	12.8	64.0	352	4	US-09-513-999C-33691	Sequence 33691, A
695	13.2	66.0	8912	4	US-08-488-446-11	Sequence 11, Appl	768	12.8	64.0	363	4	US-09-248-796A-1466	Sequence 1466, Ap
696	13.2	66.0	8912	4	US-08-467-344A-11	Sequence 11, Appl	769	12.8	64.0	369	4	US-09-543-681A-1432	Sequence 1432, Ap
697	13.2	66.0	8912	4	US-08-424-550B-11	Sequence 11, Appl	770	12.8	64.0	383	4	US-09-513-999C-34724	Sequence 34724, A
698	13.2	66.0	9143	2	US-08-639-857-32	Sequence 32, Appl	771	12.8	64.0	397	4	US-09-325-932A-130	Sequence 130, App
699	13.2	66.0	9143	4	US-08-469-260A-390	Sequence 390, App	772	12.8	64.0	417	4	US-09-615-152A-358	Sequence 358, App
700	13.2	66.0	9143	4	US-08-469-260A-393	Sequence 393, App	773	12.8	64.0	432	4	US-09-270-767-4526	Sequence 4526, Ap
701	13.2	66.0	9143	4	US-08-488-446-390	Sequence 390, App	774	12.8	64.0	432	4	US-09-270-767-19808	Sequence 19808, A
702	13.2	66.0	9143	4	US-08-488-446-393	Sequence 393, App	775	12.8	64.0	447	4	US-09-270-767-4596	Sequence 4596, Ap
703	13.2	66.0	9143	4	US-08-467-344A-390	Sequence 390, App	776	12.8	64.0	447	4	US-09-270-767-19878	Sequence 19878, A
704	13.2	66.0	9143	4	US-08-467-344A-393	Sequence 393, App	777	12.8	64.0	459	4	US-09-621-976-17642	Sequence 17642, A
705	13.2	66.0	9143	4	US-08-424-550B-390	Sequence 390, App	778	12.8	64.0	468	4	US-09-328-352-1156	Sequence 1156, Ap
706	13.2	66.0	9143	4	US-08-424-550B-393	Sequence 393, App	779	12.8	64.0	497	4	US-09-621-976-482	Sequence 482, App
707	13.2	66.0	12734	3	US-08-344-456-1	Sequence 1, Appli	780	12.8	64.0	502	4	US-09-270-767-2397	Sequence 2397, App
708	13.2	66.0	14078	3	US-09-702-330-1	Sequence 1, Appli	781	12.8	64.0	502	4	US-09-270-767-17194	Sequence 17194, Ap
709	13.2	66.0	14078	3	US-09-702-330-1	Sequence 1, Appli	782	12.8	64.0	502	4	US-09-270-767-17679	Sequence 17679, A
710	13.2	66.0	14578	3	US-08-859-694-1	Sequence 1, Appli	783	12.8	64.0	502	4	US-09-270-767-32476	Sequence 2476, A
711	13.2	66.0	16080	4	US-08-734-566A-48	Sequence 48, Appl	784	12.8	64.0	523	1	US-07-865-662F-2	Sequence 2, Appli
712	13.2	66.0	2385	4	US-08-961-527-3	Sequence 3, Appli	785	12.8	64.0	523	1	US-08-374-219B-2	Sequence 2, Appli
713	13.2	66.0	2385	4	US-08-961-527-3	Sequence 3, Appli	786	12.8	64.0	525	1	US-07-865-662F-1	Sequence 1, Appli
714	13.2	66.0	2385	4	US-08-961-527-3	Sequence 3, Appli	787	12.8	64.0	525	1	US-08-374-219B-1	Sequence 1, Appli
715	13.2	66.0	2385	4	US-08-961-527-3	Sequence 3, Appli	788	12.8	64.0	525	1	US-08-374-219B-1	Sequence 1, Appli
716	13.2	66.0	30310	1	US-08-657-346A-96	Sequence 96, Appl	789	12.8	64.0	573	3	US-09-385-982-451	Sequence 451, App
717	13.2	66.0	35100	4	US-08-306-691B-19	Sequence 19, Appl	790	12.8	64.0	573	4	US-09-328-352-2503	Sequence 2503, App
718	13.2	66.0	35100	5	PCT-US93-06251-19	Sequence 19, Appl	791	12.8	64.0	574	4	US-09-621-976-16597	Sequence 16597, A
719	13.2	66.0	35288	3	US-09-449-218D-17	Sequence 17, Appl	792	12.8	64.0	591	4	US-09-621-976-17369	Sequence 17369, A
720	13.2	66.0	35288	4	US-08-668-529A-17	Sequence 17, Appl	793	12.8	64.0	600	3	US-08-275-526C-26	Sequence 26, Appl
721	13.2	66.0	35288	4	US-08-668-529A-17	Sequence 17, Appl	794	12.8	64.0	600	3	US-08-275-526C-34	Sequence 34, Appl
722	13.2	66.0	3769	4	US-08-311-731A-23	Sequence 23, Appl	795	12.8	64.0	600	4	US-09-076-677-26	Sequence 26, Appl
723	13.2	66.0	55827	3	US-08-813-133A-3	Sequence 3, Appli	796	12.8	64.0	600	4	US-09-073-055-26	Sequence 26, Appl
c 724	13.2	66.0	111282	3	US-08-754-250-3	Sequence 3, Appli	797	12.8	64.0	600	4	US-09-073-055-34	Sequence 34, Appl
725	13.2	66.0	128779	4	US-09-497-855A-38	Sequence 38, Appl	798	12.8	64.0	606	4	US-09-248-796A-1777	Sequence 1777, Ap
726	13.2	66.0	161652	4	US-09-497-855A-40	Sequence 40, Appl	799	12.8	64.0	612	4	US-09-543-681A-616	Sequence 616, App
727	13.2	66.0	169998	4	US-08-676-610B-24	Sequence 24, Appl	800	12.8	64.0	648	4	US-09-543-681A-616	Sequence 616, App
728	13.2	66.0	197496	4	US-09-877-177A-10	Sequence 10, Appl	801	12.8	64.0	664	4	US-09-107-532A-3445	Sequence 3445, Ap
729	13.2	66.0	197496	4	US-09-877-177A-10	Sequence 10, Appl	802	12.8	64.0	664	4	US-09-221-017B-228	Sequence 228, App
730	13.2	66.0	580073	4	US-08-545-528D-1	Sequence 1, Appli	803	12.8	64.0	681	3	US-08-275-526C-30	Sequence 30, Appl
731	13.2	66.0	1230025	4	US-09-198-452A-1	Sequence 1, Appli	804	12.8	64.0	681	3	US-08-275-526C-32	Sequence 32, Appl
732	13.2	66.0	4403755	3	US-09-103-840A-2	Sequence 2, Appli	805	12.8	64.0	681	4	US-09-076-677-30	Sequence 30, Appl
733	13.2	66.0	441529	3	US-09-103-840A-1	Sequence 1, Appli	806	12.8	64.0	681	4	US-09-076-677-32	Sequence 32, Appl
734	13	65.0	309	2	US-08-633-879C-13	Sequence 13, Appl	807	12.8	64.0	681	4	US-09-073-055-30	Sequence 30, Appl
c 735	13	65.0	349	4	US-09-513-999C-467	Sequence 467, App	808	12.8	64.0	681	4	US-09-073-055-32	Sequence 32, Appl
736	13	65.0	408	3	US-08-937-271-21	Sequence 21, Appl	809	12.8	64.0	694	4	US-09-703-705-205	Sequence 205, App
737	13	65.0	1165	4	US-08-808-701A-11	Sequence 11, Appl	810	12.8	64.0	694	4	US-09-736-457-205	Sequence 205, App
738	13	65.0	1602	4	US-09-248-796A-3423	Sequence 3423, Ap	811	12.8	64.0	694	4	US-09-614-124B-205	Sequence 205, App
739	13	65.0	1769	4	US-08-580-031A-1	Sequence 1, Appli	812	12.8	64.0	694	4	US-09-671-325-205	Sequence 205, App
740	13	65.0	1865	1	US-08-592-214A-18	Sequence 18, Appl	813	12.8	64.0	694	4	US-09-583-184-205	Sequence 205, App
741	13	65.0	1865	1	US-08-149-976-18	Sequence 18, Appl	814	12.8	64.0	694	4	US-09-583-184-205	Sequence 205, App
742	13	65.0	2185	1	US-08-592-214A-19	Sequence 19, Appl	815	12.8	64.0	705	4	US-09-658-824-205	Sequence 2086, Ap
743	13	65.0	2185	3	US-08-149-976-19	Sequence 19, Appl	816	12.8	64.0	705	4	US-09-248-796A-2086	Sequence 2086, Ap
744	13	65.0	2204	3	US-09-257-799-47	Sequence 47, Appl	817	12.8	64.0	759	4	US-09-270-767-9922	Sequence 9922, Ap
745	13	65.0	2204	3	US-08-920-919A-47	Sequence 47, Appl	818	12.8	64.0	818	4	US-09-509-138-16	Sequence 16, Appl
746	13	65.0	3016	4	US-08-023-655-259	Sequence 259, App	819	12.8	64.0	879	4	US-09-248-796A-3298	Sequence 3298, Ap
747	13	65.0	11464	3	US-08-991-840A-2	Sequence 2, Appli	820	12.8	64.0	917	4	US-09-270-767-7157	Sequence 7157, Ap
748	13	65.0	43225	3	US-08-311-731A-131	Sequence 131, App	821	12.8	64.0	917	4	US-09-270-767-72439	Sequence 2439, A
749	13	65.0	43804	3	US-09-171-461-1	Sequence 1, Appli	822	12.8	64.0	928	4	US-09-152-060-46	Sequence 46, Appl
750	13	65.0	43804	3	US-09-970-711-1	Sequence 1, Appli	823	12.8	64.0	930	3	US-08-605-284B-1	Sequence 1, Appli
751	13	65.0	45716	3	US-08-965-048-5	Sequence 5, Appli	824	12.8	64.0	930	3	US-08-605-284B-2	Sequence 2, Appli
752	13	65.0	45989	3	US-08-965-048-5	Sequence 5, Appli	825	12.8	64.0	930	3	US-08-605-284B-3	Sequence 3, Appli
753	12.8	64.0	21	4	US-09-657-472-145	Sequence 145, App	826	12.8	64.0	936	4	US-08-605-284B-21	Sequence 21, Appl
754	12.8	64.0	86	4	US-08-956-171E-2070	Sequence 2070, Ap	827	12.8	64.0	960	4	US-09-543-681A-1412	Sequence 1412, Ap
755	12.8	64.0	86	4	US-08-781-986A-2070	Sequence 2070, Ap	828	12.8	64.0	960	4	US-09-270-767-27992	Sequence 27992, A
c 756	12.8	64.0	99	4	US-08-513-999C-13958	Sequence 13958, A	829	12.8	64.0	1001	4	US-09-778-898A-4	Sequence 4, Appli
c 757	12.8	64.0	162	4	US-09-509-138-15	Sequence 15, Appli	830	12.8	64.0	1022	3	US-08-275-526C-1	Sequence 1, Appli

C 831	12.8	64.0	1022	3	US-08-275-526C-35	Sequence 35, Appl	C 904	12.8	64.0	2907	3	US-09-335-411-55	Sequence 55, Appl
C 832	12.8	64.0	1022	4	US-09-076-677-1	Sequence 1, Appl	905	12.8	64.0	3001	4	US-09-335-411-55	Sequence 221, Appl
C 833	12.8	64.0	1022	4	US-09-076-677-35	Sequence 35, Appl	906	12.8	64.0	3023	3	US-09-593-589-10	Sequence 10, Appl
C 834	12.8	64.0	1022	4	US-09-073-055-1	Sequence 1, Appl	c 907	12.8	64.0	3046	4	US-09-710-279-4050	Sequence 4050, Ap
C 835	12.8	64.0	1022	4	US-09-073-055-35	Sequence 35, Appl	908	12.8	64.0	3115	4	US-09-702-705-802	Sequence 802, App
C 836	12.8	64.0	1022	4	US-09-134-001C-872	Sequence 872, Appl	909	12.8	64.0	3115	4	US-09-736-457-802	Sequence 802, App
C 837	12.8	64.0	1023	3	US-09-252-991A-4116	Sequence 4116, Ap	910	12.8	64.0	3115	4	US-09-614-124B-802	Sequence 802, App
C 838	12.8	64.0	1053	4	US-09-270-767-10421	Sequence 10421, A	911	12.8	64.0	3115	4	US-09-671-325-802	Sequence 802, App
C 839	12.8	64.0	1058	4	US-09-489-039A-3456	Sequence 3456, A	912	12.8	64.0	3115	4	US-09-589-184-802	Sequence 802, App
C 840	12.8	64.0	1080	4	US-09-489-039A-3456	Sequence 109, App	913	12.8	64.0	3115	4	US-09-658-824-802	Sequence 802, App
C 841	12.8	64.0	1083	4	US-09-540-236-109	Sequence 109, App	914	12.8	64.0	3123	4	US-09-711-164-271	Sequence 271, App
C 842	12.8	64.0	1188	3	US-09-134-001C-623	Sequence 623, App	C 914	12.8	64.0	3123	4	US-09-711-164-271	Sequence 271, App
C 843	12.8	64.0	1194	4	US-09-252-991A-4097	Sequence 4097, App	C 915	12.8	64.0	3123	4	US-09-492-709A-122	Sequence 122, App
C 844	12.8	64.0	1203	4	US-09-561-763-12	Sequence 12, Appl	916	12.8	64.0	3126	3	US-08-898-978-1	Sequence 1, Appl
C 845	12.8	64.0	1203	4	US-09-431-367B-12	Sequence 12, Appl	917	12.8	64.0	3126	3	US-09-372-858-1	Sequence 1, Appl
C 846	12.8	64.0	1205	3	US-09-120-772-1	Sequence 1, Appl	918	12.8	64.0	3131	1	US-08-162-809-1	Sequence 1, Appl
C 847	12.8	64.0	1233	4	US-09-543-681A-1235	Sequence 1235, Ap	919	12.8	64.0	3133	1	US-07-865-662F-7	Sequence 7, Appl
C 848	12.8	64.0	1242	4	US-09-543-681A-1863	Sequence 1863, Ap	920	12.8	64.0	3134	1	US-07-865-662F-7	Sequence 7, Appl
C 849	12.8	64.0	1255	4	US-09-270-767-12251	Sequence 12251, A	921	12.8	64.0	3134	3	US-08-374-219B-7	Sequence 7, Appl
C 850	12.8	64.0	1260	4	US-09-248-796A-453	Sequence 453, App	922	12.8	64.0	3149	4	US-09-710-279-3902	Sequence 3902, Ap
C 851	12.8	64.0	1296	4	US-09-489-039A-5508	Sequence 5508, Ap	923	12.8	64.0	3501	1	US-08-448-170-5	Sequence 5, Appl
C 852	12.8	64.0	1329	4	US-09-248-796A-12354	Sequence 12354, A	924	12.8	64.0	3501	3	US-08-961-803-4	Sequence 4, Appl
C 853	12.8	64.0	1341	4	US-09-107-532A-203	Sequence 203, App	925	12.8	64.0	3507	4	US-08-661-322A-21	Sequence 21, Appl
C 854	12.8	64.0	1393	4	US-09-710-279-2725	Sequence 2725, Ap	926	12.8	64.0	3742	4	US-09-016-434-1370	Sequence 1370, Ap
C 855	12.8	64.0	1413	4	US-09-016-434-1275	Sequence 1275, Ap	927	12.8	64.0	3796	2	US-08-762-308-11	Sequence 11, Appl
C 856	12.8	64.0	1506	4	US-09-561-763-10	Sequence 10, Appl	928	12.8	64.0	3796	4	US-09-844-634-10	Sequence 10, Appl
C 857	12.8	64.0	1506	4	US-09-431-367B-10	Sequence 10, Appl	929	12.8	64.0	3813	2	US-08-650-000-3	Sequence 3, Appl
C 858	12.8	64.0	1509	4	US-09-540-236-1860	Sequence 1860, Ap	930	12.8	64.0	3813	4	US-09-758-124-3	Sequence 3, Appl
C 859	12.8	64.0	1532	4	US-09-270-767-12796	Sequence 12796, A	931	12.8	64.0	3813	6	539560-3	Patent No. 539560
C 860	12.8	64.0	1537	4	US-09-620-312D-561	Sequence 561, App	932	12.8	64.0	4094	1	US-08-571-758-5	Sequence 5, Appl
C 861	12.8	64.0	1557	4	US-09-248-796A-5091	Sequence 5091, Ap	933	12.8	64.0	4094	1	US-08-909-984A-5	Sequence 5, Appl
C 862	12.8	64.0	1626	4	US-09-614-221A-521	Sequence 521, App	934	12.8	64.0	4094	1	US-08-909-984A-5	Sequence 5, Appl
C 863	12.8	64.0	1712	3	US-09-302-620B-105	Sequence 105, App	935	12.8	64.0	4253	2	US-08-691-814B-7	Sequence 7, Appl
C 864	12.8	64.0	1712	4	US-09-912-161-45	Sequence 45, Appl	936	12.8	64.0	4304	3	US-08-368-776A-1	Sequence 1, Appl
C 865	12.8	64.0	1712	4	US-09-911-781-23	Sequence 23, Appl	937	12.8	64.0	4304	5	PCT-US96-00419-1	Sequence 1, Appl
C 866	12.8	64.0	1720	4	US-10-400-902-23	Sequence 23, Appl	938	12.8	64.0	4380	1	US-07-582-945-1	Sequence 1, Appl
C 867	12.8	64.0	1720	4	US-09-205-258-133	Sequence 133, App	939	12.8	64.0	4380	2	US-08-453-141-1	Sequence 1, Appl
C 868	12.8	64.0	1761	4	US-09-339-159B-9	Sequence 9, Appl	940	12.8	64.0	4380	3	US-08-293-314-1	Sequence 1, Appl
C 869	12.8	64.0	1762	1	US-07-870-029-1	Sequence 1, Appl	941	12.8	64.0	4399	4	US-09-911-781-27	Sequence 27, Appl
C 870	12.8	64.0	1815	1	US-09-328-475C-339	Sequence 339, App	942	12.8	64.0	4399	4	US-10-400-902-27	Sequence 27, Appl
C 871	12.8	64.0	1816	1	US-07-865-662F-5	Sequence 5, Appl	943	12.8	64.0	4637	4	US-09-702-705-804	Sequence 804, App
C 872	12.8	64.0	1822	1	US-07-865-662F-6	Sequence 6, Appl	944	12.8	64.0	4637	4	US-09-736-457-804	Sequence 804, App
C 873	12.8	64.0	1822	3	US-08-374-219B-6	Sequence 6, Appl	945	12.8	64.0	4637	4	US-09-614-124B-804	Sequence 804, App
C 874	12.8	64.0	1858	4	US-09-336-536-56	Sequence 56, Appl	946	12.8	64.0	4637	4	US-09-589-184-804	Sequence 804, App
C 875	12.8	64.0	1881	3	US-09-134-001C-489	Sequence 489, App	947	12.8	64.0	4637	4	US-09-658-824-804	Sequence 804, App
C 876	12.8	64.0	1957	3	US-09-352-990-11	Sequence 11, Appl	948	12.8	64.0	5257	4	US-09-023-655-1401	Sequence 1401, Ap
C 877	12.8	64.0	2094	4	US-09-369-247-46	Sequence 46, Appl	949	12.8	64.0	5257	4	US-09-917-254-47	Sequence 47, Appl
C 878	12.8	64.0	2139	3	US-09-189-527-3	Sequence 3, Appl	950	12.8	64.0	5261	1	US-08-045-806-3	Sequence 3, Appl
C 879	12.8	64.0	2143	4	US-09-270-767-13897	Sequence 13897, A	951	12.8	64.0	5261	1	US-08-366-051B-3	Sequence 3, Appl
C 880	12.8	64.0	2163	4	US-09-543-681A-1566	Sequence 1566, Ap	952	12.8	64.0	5261	1	US-08-188-582-10	Sequence 10, Appl
C 881	12.8	64.0	2272	1	US-08-233-005-1	Sequence 1, Appl	953	12.8	64.0	5962	1	US-08-646-715-10	Sequence 10, Appl
C 882	12.8	64.0	2272	1	US-08-428-943-1	Sequence 1, Appl	954	12.8	64.0	5962	1	US-08-306-691B-42	Sequence 42, Appl
C 883	12.8	64.0	2272	3	PCT-US95-04858-1	Sequence 1, Appl	955	12.8	64.0	7011	1	US-08-478-507-10	Sequence 10, Appl
C 884	12.8	64.0	2272	5	US-08-246-403A-7	Sequence 7, Appl	956	12.8	64.0	7171	3	US-08-478-507-10	Sequence 10, Appl
C 885	12.8	64.0	2316	1	US-08-246-403A-10	Sequence 10, Appl	957	12.8	64.0	7171	3	US-09-128-275A-10	Sequence 10, Appl
C 886	12.8	64.0	2316	1	US-08-710-279-4408	Sequence 4408, Ap	958	12.8	64.0	7171	3	US-09-553-427-10	Sequence 10, Appl
C 887	12.8	64.0	2328	2	US-08-849-536A-3	Sequence 3, Appl	959	12.8	64.0	7280	4	US-09-821-726A-14	Sequence 14, Appl
C 888	12.8	64.0	2445	4	US-09-339-159B-25	Sequence 25, Appl	960	12.8	64.0	11558	5	PCT-US93-06251-23	Sequence 23, Appl
C 889	12.8	64.0	2490	4	US-09-976-594-361	Sequence 361, App	961	12.8	64.0	16011	4	US-09-600-319-3	Sequence 3, Appl
C 890	12.8	64.0	2578	4	US-10-101-464A-857	Sequence 857, App	962	12.8	64.0	31147	4	US-09-596-002-25	Sequence 25, Appl
C 891	12.8	64.0	2652	4	US-09-489-039A-5584	Sequence 5584, Ap	963	12.8	64.0	32798	4	US-09-604-694B-1	Sequence 1, Appl
C 892	12.8	64.0	2667	4	US-09-673-395A-117	Sequence 117, App	964	12.8	64.0	32798	4	US-09-596-002-19	Sequence 19, Appl
C 893	12.8	64.0	2667	4	US-09-673-395A-117	Sequence 117, App	965	12.8	64.0	34303	2	US-08-735-609-4	Sequence 4, Appl
C 894	12.8	64.0	2750	4	US-10-140-002-85	Sequence 85, Appl	966	12.8	64.0	34303	2	US-08-735-609-4	Sequence 4, Appl
C 895	12.8	64.0	2853	3	US-09-556-601-25	Sequence 25, Appl	967	12.8	64.0	34303	3	US-09-244-752-4	Sequence 4, Appl
C 896	12.8	64.0	2858	3	US-08-816-346-3	Sequence 3, Appl	968	12.8	64.0	34303	3	US-09-245-497-4	Sequence 4, Appl
C 897	12.8	64.0	2858	3	US-08-816-346-3	Sequence 3, Appl	969	12.8	64.0	34303	4	US-09-562-919-4	Sequence 4, Appl
C 898	12.8	64.0	2858	3	US-09-335-411-3	Sequence 3, Appl	970	12.8	64.0	34382	2	US-09-374-483-6	Sequence 6, Appl
C 899	12.8	64.0	2859	2	US-08-788-674-7	Sequence 7, Appl	971	12.8	64.0	35408	3	US-08-973-334-3	Sequence 3, Appl
C 900	12.8	64.0	2859	2	US-08-788-674-7	Sequence 7, Appl	972	12.8	64.0	35408	3	US-09-563-869A-3	Sequence 3, Appl
C 901	12.8	64.0	2907	3	US-08-816-346-1	Sequence 1, Appl	973	12.8	64.0	35408	3	US-08-549-489-3	Sequence 3, Appl
C 902	12.8	64.0	2907	3	US-08-816-346-55	Sequence 55, Appl	974	12.8	64.0	35871	2	US-09-956-335-2	Sequence 2, Appl
C 903	12.8	64.0	2907	3	US-08-335-411-1	Sequence 1, Appl	975	12.8	64.0	35935	2	US-08-735-609-1	Sequence 1, Appl
C 904	12.8	64.0	2907	3	US-08-335-411-1	Sequence 1, Appl	976	12.8	64.0	35935	2	US-08-735-609-1	Sequence 1, Appl

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c 994 12.8 64.0 202001 4 US-09-734-674-3  
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c 996 12.6 63.0 38 3 US-09-355-434-15  
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c 998 12.6 63.0 50 3 US-09-206-903A-6  
c 999 12.6 63.0 50 3 US-09-202-122-6  
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## ALIGNMENTS

RESULT 1  
US-09-789-300A-1  
; Sequence 1, Application US/09789300A  
; Patent No. 6458576  
; GENERAL INFORMATION:  
; APPLICANT: Meyers, Rachel  
; APPLICANT: Rudolph-Owen, Laura A.  
; TITLE OF INVENTION: 22406, A No. 6458576el Human Pyridoxal-Phosphate  
; FILE OF INVENTION: Dependent Enzyme Family Member and Uses Therefore  
; FILE REFERENCE: 35800/208926  
; CURRENT APPLICATION NUMBER: US/09/789,300A  
; CURRENT FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: US 60/183,208  
; PRIOR FILING DATE: 2000-02-17  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1770  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: {69}...(1091)  
US-09-789-300A-1  
Query Match 80.0%; Score 16; DB 4; Length 1770;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 TTAATGGAGAGTGCT 20  
Db 1183 TTAATGGAGAGTGCT 1198  
RESULT 2  
US-09-328-352-21/c  
; Sequence 21, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352

; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 21  
; LENGTH: 318  
; TYPE: DNA  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-21  
Query Match 79.0%; Score 15.8; DB 4; Length 318;  
Best Local Similarity 89.5%; Pred. No. 37;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GCAGTTAATGGAGAGTGCC 19  
Db 240 GCGTTAATGAAGAGTGCC 222  
RESULT 3  
US-09-328-352-24  
; Sequence 24, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 24  
; LENGTH: 351  
; TYPE: DNA  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-24  
Query Match 79.0%; Score 15.8; DB 4; Length 351;  
Best Local Similarity 89.5%; Pred. No. 37;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GCAGTTAATGGAGAGTGCC 19  
Db 97 GCGTTAATGAAGAGTGCC 115  
RESULT 4  
US-09-302-769-20/c  
; Sequence 20, Application US/09302769  
; Patent No. 6323317  
; GENERAL INFORMATION:  
; APPLICANT: HILTON, Douglas J  
; APPLICANT: ALEXANDER, Warren S  
; APPLICANT: VINEY, Elizabeth M  
; APPLICANT: WILSON, Tracey A  
; APPLICANT: RICHARDSON, Rachael T  
; APPLICANT: STARR, Robyn  
; APPLICANT: NICHOLSON, Sandra E  
; APPLICANT: METCALF, Donald  
; APPLICANT: NICOLA, Nicos A  
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC AGENTS  
; FILE REFERENCE: 10976Z  
; CURRENT APPLICATION NUMBER: US/09/302,769  
; CURRENT FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: 08/962,560  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 2369  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: {116}...(1327)

## US-09-302-769-20

Query Match 79.0%; Score 15.8; DB 3; Length 2369;  
Best Local Similarity 89.5%; Pred. No. 56;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGGCT 20  
|||||  
DB 1626 CAGTTAAGGAGGTGGCT 1608

## RESULT 5

US-09-058-489-19  
; Sequence 19, Application US/09058489  
; Patent No. 6103886  
; GENERAL INFORMATION:  
; APPLICANT: Whitehead Institute for Biomedical Research  
; APPLICANT: Lahn, Bruce  
; APPLICANT: Page, David  
; TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of  
; FILE REFERENCE: WHI97-08pA  
; CURRENT APPLICATION NUMBER: US/09/058,489  
; CURRENT FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/041,877  
; EARLIER FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 19  
; LENGTH: 4335  
; TYPE: DNA  
; ORGANISM: Human  
US-09-058-489-19

Query Match 79.0%; Score 15.8; DB 3; Length 4335;  
Best Local Similarity 89.5%; Pred. No. 64;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGGCT 20  
|||||  
DB 3404 CAGTCAATGGAGAGGGCT 3422

## RESULT 6

US-09-058-489-20  
; Sequence 20, Application US/09058489  
; Patent No. 6103886  
; GENERAL INFORMATION:  
; APPLICANT: Whitehead Institute for Biomedical Research  
; APPLICANT: Lahn, Bruce  
; APPLICANT: Page, David  
; TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of  
; FILE REFERENCE: WHI97-08pA  
; CURRENT APPLICATION NUMBER: US/09/058,489  
; CURRENT FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/041,877  
; EARLIER FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 20  
; LENGTH: 4931  
; TYPE: DNA  
; ORGANISM: Human  
US-09-058-489-20

Query Match 79.0%; Score 15.8; DB 3; Length 4931;  
Best Local Similarity 89.5%; Pred. No. 66;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGGCT 20  
|||||  
DB 3404 CAGTCAATGGAGAGGGCT 3422

## RESULT 7

US-09-058-489-21  
; Sequence 21, Application US/09058489  
; Patent No. 6103886  
; GENERAL INFORMATION:  
; APPLICANT: Whitehead Institute for Biomedical Research  
; APPLICANT: Lahn, Bruce  
; APPLICANT: Page, David  
; TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of  
; FILE REFERENCE: WHI97-08pA  
; CURRENT APPLICATION NUMBER: US/09/058,489  
; CURRENT FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/041,877  
; EARLIER FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 21  
; LENGTH: 6476  
; TYPE: DNA  
; ORGANISM: Human  
US-09-058-489-21

Query Match 79.0%; Score 15.8; DB 3; Length 6476;  
Best Local Similarity 89.5%; Pred. No. 69;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGGCT 20  
|||||  
DB 3404 CAGTCAATGGAGAGGGCT 3422

## RESULT 8

US-09-227-357-38/c  
; Sequence 38, Application US/09227357  
; Patent No. 6342581  
; GENERAL INFORMATION:  
; APPLICANT: Fischer et al.  
; TITLE OF INVENTION: 123 Human Secreted Proteins  
; FILE REFERENCE: P2010P1  
; CURRENT APPLICATION NUMBER: US/09/227,357  
; CURRENT FILING DATE: 1999-01-08  
; EARLIER APPLICATION NUMBER: PCT/US98/13684  
; EARLIER FILING DATE: 1998-07-07  
; EARLIER APPLICATION NUMBER: 60/051,926  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/052,793  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,925  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,929  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/052,803  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/052,732  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,931  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,932  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,916  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,930  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,918  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,920  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/052,733  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/052,795

EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,919  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,928  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,928  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/055,722  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,723  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,948  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,949  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,953  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,950  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,947  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,964  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/056,360  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,684  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,984  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,954  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/058,785  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,664  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,660  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,661  
EARLIER FILING DATE: 1997-09-12  
NUMBER OF SEQ ID NOS: 672  
SOFTWARE: Patent in Ver. 2.0  
SEQ ID NO 38  
LENGTH: 1122  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (380)  
OTHER INFORMATION: n equals a,t,g, or c  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (381)  
OTHER INFORMATION: n equals a,t,g, or c  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (402)  
OTHER INFORMATION: n equals a,t,g, or c  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (499)  
OTHER INFORMATION: n equals a,t,g, or c  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (505)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-227-357-38

Query Match 77.0%; Score 15.4; DB 3; Length 1122;  
Best Local Similarity 94.1%; Pred. No. 78;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAGTTAATGGAGAGTG 17  
Db 741 GCAGTTAATGGAGAGTG 725

RESULT 9  
US-09-735-935-3/c  
Sequence 3, Application US/09735935  
Patent No. 6420150  
GENERAL INFORMATION:  
APPLICANT: GUEGLER, Karl et al  
TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING  
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN  
TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS,  
TITLE OF INVENTION: AND USES THEREOF  
FILE REFERENCE: CL000970  
CURRENT APPLICATION NUMBER: US/09/735,935  
CURRENT FILING DATE: 2000-12-14  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 5044  
TYPE: DNA  
ORGANISM: Human  
US-09-735-935-3

Query Match 77.0%; Score 15.4; DB 4; Length 5044;  
Best Local Similarity 94.1%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CAGTTAATGGAGAGTG 18  
Db 231 CAGTTAATGGAGAGTG 215

RESULT 10  
US-10-162-639-3/c  
Sequence 3, Application US/10162639  
Patent No. 6730505  
GENERAL INFORMATION:  
APPLICANT: GUEGLER, Karl et al  
TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING  
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN  
TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS, AND USES THEREOF  
FILE REFERENCE: CL000970DIV  
CURRENT APPLICATION NUMBER: US/10/162,639  
CURRENT FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: 60/252,895  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 09/735,935  
PRIOR FILING DATE: 2000-12-14  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 5044  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-162-639-3

Query Match 77.0%; Score 15.4; DB 4; Length 5044;  
Best Local Similarity 94.1%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CAGTTAATGGAGAGTG 18  
Db 231 CAGTTAATGGAGAGTG 215

RESULT 11  
US-09-839-477-7  
Sequence 7, Application US/09839477  
Patent No. 6723895  
GENERAL INFORMATION:  
APPLICANT: Shorosh, Basil S.  
APPLICANT: DeBonte, Lorin R.  
TITLE OF INVENTION: PLANTS CONTAINING A CYTOSOLIC ACETYL  
TITLE OF INVENTION: COA-CARBOXYLASE

```

; FILE REFERENCE: 07148-094001
; CURRENT APPLICATION NUMBER: US/09/839,477
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 60/198,794
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 7151
; TYPE: DNA
; ORGANISM: Medicago sativa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(6771)
; US-09-839-477-7

```

```

Query Match 77.0%; Score 15.4; DB 4; Length 7151;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 4 GTTAATCGAGAGTGCT 20
Db 5584 GTTAATCGAAAGTGCT 5600

```

# RESULT 12

```

US-09-816-095-3/c
; Sequence 3, Application US/09816095
; Patent No. 6664084
; GENERAL INFORMATION:
; APPLICANT: GAN, Weinliu
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: C1001147
; CURRENT APPLICATION NUMBER: US/09/816,095
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 99916
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(99916)
; OTHER INFORMATION: n = A,T,C or G
; US-09-816-095-3

```

```

Query Match 77.0%; Score 15.4; DB 4; Length 99916;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 2 CAGTTAATCGAGAGTGG 18
Db 15704 CAGTTAATCGAGAGTGG 15688

```

# RESULT 13

```

US-10-027-983-11
; Sequence 11, Application US/10027983
; Patent No. 6617182
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Mark P. Roach
; TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR ALPHA EXPRESSION
; FILE REFERENCE: RTS-0340
; CURRENT APPLICATION NUMBER: US/10/027,983
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 11
; LENGTH: 392000
; TYPE: DNA

```

```

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 137740
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 137742
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (138122)...(138221)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 145507
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 151967
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (151967)...(1542066)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 154217
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (164037)...(164136)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (174557)...(174756)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (186224)...(186323)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (195342)...(195341)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 202703
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (202771)...(202870)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (206246)...(215602)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (218126)...(218225)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (220350)...(220459)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (222717)...(222816)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (223981)...(224080)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (227487)...(227586)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (230157)...(230256)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (232299)...(232398)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (236552)...(236651)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (238789)...(248788)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: exon
; LOCATION: (118288)...(119101)

```

OTHER INFORMATION: exon 1C  
NAME/KEY: exon:intron junction  
LOCATION: (151129)...(151130)  
OTHER INFORMATION: exon 5:intron 5  
NAME/KEY: exon:intron junction  
LOCATION: (299248)...(299249)  
OTHER INFORMATION: exon 9:intron 9  
NAME/KEY: exon:intron junction  
LOCATION: (348578)...(348579)  
OTHER INFORMATION: exon 10:intron 10  
NAME/KEY: intron  
LOCATION: (348579)...(381838)  
OTHER INFORMATION: intron 10  
NAME/KEY: intron:exon junction  
LOCATION: (386185)...(386186)  
OTHER INFORMATION: intron 11:exon 12  
US-10-027-983-11

Query Match 77.0%; Score 15.4; DB 4; Length 392000;  
Best Local Similarity 94.1%; Pred. No. 2.5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTG 17  
DB 375282 GCTGTTAATGGAGAGTG 375298

## RESULT 14

US-09-638-202A-21/c  
Sequence 21, Application US/09638202A  
Patent No. 6462189  
GENERAL INFORMATION:  
APPLICANT: Koieda, Shohei  
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
NUMBER OF SEQUENCES: 118  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
STREET: 121 South Eighth Street, Ste. 1600  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0b

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/638, 202A  
FILING DATE: 11-Aug-2000

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/096, 749  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Ann S. Viksnins  
REGISTRATION NUMBER: 37,748  
REFERENCE/DOCKET NUMBER: 109.034US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (612) 373-6900  
TELEFAX: (612) 339-3061

INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: <Unknown>

ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 21:  
US-09-638-202A-21

Query Match 76.0%; Score 15.2; DB 4; Length 35;  
Best Local Similarity 85.0%; Pred. No. 48;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGCT 20  
DB 32 GTAGTTAATCGAGATTGGCT 13

## RESULT 15

US-09-096-749A-21/c  
Sequence 21, Application US/09096749A  
Patent No. 6673901  
GENERAL INFORMATION:  
APPLICANT: Koieda, Shohei  
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
NUMBER OF SEQUENCES: 118  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
STREET: 121 South Eighth Street, Ste. 1600  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0b

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/096, 749A  
FILING DATE: June 12, 1998

PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Ann S. Viksnins  
REGISTRATION NUMBER: 37,748  
REFERENCE/DOCKET NUMBER: 109.034US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (612) 373-6900  
TELEFAX: (612) 339-3061

INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:

US-09-096-749A-21

Query Match 76.0%; Score 15.2; DB 4; Length 35;  
Best Local Similarity 85.0%; Pred. No. 48;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGCT 20  
DB 32 GTAGTTAATCGAGATTGGCT 13

## RESULT 16

US-09-637-614-21/c  
Sequence 21, Application US/09637614  
Patent No. 6703199  
GENERAL INFORMATION:  
APPLICANT: Koieda, Shohei  
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
NUMBER OF SEQUENCES: 118



;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
;/ STREET: 121 South Eighth Street, Ste. 1600  
;/ CITY: Minneapolis  
;/ STATE: MN  
;/ COUNTRY: USA  
;/ ZIP: 55402  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Diskette  
;/ COMPUTER: IBM Compatible  
;/ OPERATING SYSTEM: DOS  
;/ SOFTWARE: FastSeq Version 2.0b  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/09/637,614  
;/ FILING DATE: 11-Aug-2000  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 09/096,749  
;/ FILING DATE: <Unknown>  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Ann S. Viksnins  
;/ REGISTRATION NUMBER: 37,748  
;/ REFERENCE/DOCKET NUMBER: 109.034US1  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (612) 373-6900  
;/ TELEFAX: (612) 339-3061  
;/ INFORMATION FOR SEQ ID NO: 21:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 35 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: cDNA  
;/ HYPOTHETICAL: NO  
;/ ANTI-SENSE: NO  
;/ FRAGMENT TYPE: <Unknown>  
;/ ORIGINAL SOURCE:  
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 21:  
;/ US-09-637-614-21

Query Match 76.0%; Score 15.2; DB 4; Length 35;  
Best Local Similarity 85.0%; Pred.No. 48;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAGTTAATCGAGATGGCT 20  
Db 32 GTAGTTAATCGAGATGGCT 13

RESULT 17  
US-09-638-202A-111/c  
; Sequence 111, Application US/09638202A  
; Patent No. 6462189  
; GENERAL INFORMATION:  
; APPLICANT: Koleda, Shohel  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
; STREET: 121 South Eighth Street, Ste. 1600  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/638,202A  
; FILING DATE: 11-Aug-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/096,749

;/ FILING DATE: <Unknown>  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Ann S. Viksnins  
;/ REGISTRATION NUMBER: 37,748  
;/ REFERENCE/DOCKET NUMBER: 109.034US1  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (612) 373-6900  
;/ TELEFAX: (612) 339-3061  
;/ INFORMATION FOR SEQ ID NO: 111:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 308 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: cDNA  
;/ HYPOTHETICAL: NO  
;/ ANTI-SENSE: NO  
;/ FRAGMENT TYPE: <Unknown>  
;/ ORIGINAL SOURCE:  
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 111:  
;/ US-09-638-202A-111

Query Match 76.0%; Score 15.2; DB 4; Length 308;  
Best Local Similarity 85.0%; Pred.No. 76;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAGTTAATCGAGATGGCT 20  
Db 285 GTAGTTAATCGAGATGGCT 266

RESULT 18  
US-09-096-749A-111/c  
; Sequence 111, Application US/09096749A  
; Patent No. 6673901  
; GENERAL INFORMATION:  
; APPLICANT: Koleda, Shohel  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
; STREET: 121 South Eighth Street, Ste. 1600  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/096,749A  
; FILING DATE: June 12, 1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ann S. Viksnins  
; REGISTRATION NUMBER: 37,748  
; REFERENCE/DOCKET NUMBER: 109.034US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (612) 373-6900  
; TELEFAX: (612) 339-3061  
; INFORMATION FOR SEQ ID NO: 111:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 308 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO

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; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-09-096-749A-111

Query Match          76.0%; Score 15.2; DB 4; Length 308;
Best Local Similarity 85.0%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAGTTAATCGAGATGGCT 20
Db 285 GTAGTTAATCGAGATGGCT 266

RESULT 19
US-09-637-614-111/c
; Sequence 111, Application US/09637614
; Patent No. 6703199
; GENERAL INFORMATION:
; APPLICANT: Koieda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/637,614
; FILING DATE: 11-Aug-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/096,749
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Vikensins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 308 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-09-637-614-111

Query Match          76.0%; Score 15.2; DB 4; Length 308;
Best Local Similarity 85.0%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAGTTAATCGAGATGGCT 20
Db 285 GTAGTTAATCGAGATGGCT 266

RESULT 20
US-08-689-421-20/c
; Sequence 20, Application US/08689421
; Patent No. 6008029
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie S.
; APPLICANT: Brown, Kimberley M.
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Halkier, Torben P
; TITLE OF INVENTION: PURIFIED COPRINUS LACCASES AND NUCLEIC ACIDS
; TITLE OF INVENTION: PURIFIED COPRINUS LACCASES AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 62074300 No. 62074300disk of No. 6207430th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie S.
; APPLICANT: Brown, Kimberley M.
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Halkier, Torben P
; TITLE OF INVENTION: PURIFIED COPRINUS LACCASES AND NUCLEIC ACIDS
; TITLE OF INVENTION: PURIFIED COPRINUS LACCASES AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 60080290 No. 6008029disk of No. 6008029th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,421
; FILING DATE: 9-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 4554.204-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1170 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1170
US-08-689-421-20

Query Match          76.0%; Score 15.2; DB 3; Length 1170;
Best Local Similarity 85.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAGTTAATCGAGATGGCT 20
Db 856 GCGTTGATGGAAGTGGCT 837

RESULT 21
US-09-389-528-20/c
; Sequence 20, Application US/09389528
; Patent No. 6207430
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie S.
; APPLICANT: Brown, Kimberley M.
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Halkier, Torben P
; TITLE OF INVENTION: PURIFIED COPRINUS LACCASES AND NUCLEIC ACIDS
; TITLE OF INVENTION: PURIFIED COPRINUS LACCASES AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 62074300 No. 6207430disk of No. 6207430th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/389,528  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/689,421  
; FILING DATE: 9-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Harrington, James J.  
; REGISTRATION NUMBER: 38,711  
; REFERENCE/DOCKET NUMBER: 4554.204-WO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-867-0123  
; TELEFAX: 212-878-9655  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1170 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1170  
US-09-389-528-20

Query Match 76.0%; Score 15.2; DB 3; Length 1170;  
Best Local Similarity 85.0%; Pred. No. 1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

Qy 1 GCAGTTAATGGAGAGTGGCT 20  
Db 856 GCGGTTGATGGAAGTGGCT 837

## RESULT 22

US-09-181-827A-20/c  
; Sequence 20, Application US/09181827A  
; Patent No. 6242232  
; GENERAL INFORMATION:  
; APPLICANT: Yaver, Debbie S.  
; APPLICANT: Brown, Kimberly M.  
; APPLICANT: Kauppinen, Sakari  
; APPLICANT: Halkier, Torben P.  
; TITLE OF INVENTION: Purified Coprinus Laccases And Nucleic  
; TITLE OF INVENTION: Acids Encoding Same  
; FILE REFERENCE: 4554.200-US  
; CURRENT APPLICATION NUMBER: US/09/181,827A  
; CURRENT FILING DATE: 1998-10-28  
; PRIOR APPLICATION NUMBER: 60/002,800  
; PRIOR FILING DATE: 1995-08-25  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 1170  
; TYPE: DNA  
; ORGANISM: Coprinus cinereus  
US-09-181-827A-20

Query Match 76.0%; Score 15.2; DB 3; Length 1170;  
Best Local Similarity 85.0%; Pred. No. 1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

Qy 1 GCAGTTAATGGAGAGTGGCT 20  
Db 856 GCGGTTGATGGAAGTGGCT 837

## RESULT 23

US-09-489-039A-4503

; Sequence 4503, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 4503  
; LENGTH: 1305  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-4503

Query Match 76.0%; Score 15.2; DB 4; Length 1305;  
Best Local Similarity 85.0%; Pred. No. 1e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAGTTAATGGAGAGTGGCT 20  
Db 531 GCAGTTTATTGAGAGCGGCT 550

## RESULT 24

US-09-489-039A-3898  
; Sequence 3898, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 3898  
; LENGTH: 1332  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-3898

Query Match 76.0%; Score 15.2; DB 4; Length 1332;  
Best Local Similarity 85.0%; Pred. No. 1e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAGTTAATGGAGAGTGGCT 20  
Db 582 GCAGTTTATTGAGAGTGGGCT 601

## RESULT 25

US-09-799-451-771/c  
; Sequence 771, Application US/09799451  
; Patent No. 6783989  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Zhou, Ping  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Zhang, Jie  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Ma, Yunging  
; APPLICANT: Yamazaki, Victoria  
; APPLICANT: Chen, Rui-hong

APPLICANT: Wang, Zhiwei  
APPLICANT: Wang, Dunrui  
APPLICANT: Yang, Yungchong  
APPLICANT: Wehrman, Tom  
APPLICANT: Ghosh, Reena  
APPLICANT: Dmanac, Radoje T.  
TITLE OF INVENTION: No. 678969el Nucleic Acids and  
FILE REFERENCE: Polypeptides  
FILE REFERENCE: 803  
CURRENT APPLICATION NUMBER: US/09/799,451  
CURRENT FILING DATE: 2001-03-05  
NUMBER OF SEQ ID NOS: 948  
SOFTWARE: pt\_FL\_genes Version 2.0  
SEQ ID NO 771  
LENGTH: 2590  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (190)..(2223)  
US-09-799-451-771

Query Match 76.0%; Score 15.2; DB 4; Length 2590;  
Best Local Similarity 85.0%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGCGT 20  
DB 1866 GCAGTTGATGCAGAGTAGCT 1847

RESULT 26  
US-08-689-421-32/c  
Sequence 32, Application US/08689421  
Patent No. 6008029  
GENERAL INFORMATION:  
APPLICANT: Yaver, Debbie S.  
APPLICANT: Brown, Kimberley M.  
APPLICANT: Kauppinen, Sakari  
APPLICANT: Halkier, Torben P  
TITLE OF INVENTION: PURIFIED COPRINUS LACCASES AND NUCLEIC ACIDS  
TITLE OF INVENTION: ENCODING SAME  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6008029o No. 6008029disk of No. 6008029th America, Inc.  
STREET: 405 Lexington Avenue, 64th Floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/689,421  
FILING DATE: 9-AUG-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Harrington, James J.  
REGISTRATION NUMBER: 38,711  
REFERENCE/DOCKET NUMBER: 4554.204-WO  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3566 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(456..578, 631..696, 746..814, 869..1015,  
1069..1140, 1199..1213, 1271..1300, 1366..1563,  
1622..2149, 2213..2233, 2303..2452, 2514..2537,  
2598..2654, 2725..2776)  
US-09-389-528-32

Query Match 76.0%; Score 15.2; DB 3; Length 3566;  
Best Local Similarity 85.0%; Pred. No. 1.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

FEATURE:  
NAME/KEY: CDS  
LOCATION: join(456..578, 631..696, 746..814, 869..1015,  
1069..1140, 1199..1213, 1271..1300, 1366..1563,  
1622..2149, 2213..2233, 2303..2452, 2514..2537,  
2598..2654, 2725..2776)  
US-08-689-421-32

Query Match 76.0%; Score 15.2; DB 3; Length 3566;  
Best Local Similarity 85.0%; Pred. No. 1.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGCGT 20  
DB 2015 GCGGTGATGGAAGTGCGT 1996

RESULT 27  
US-09-389-528-32/c  
Sequence 32, Application US/09389528  
Patent No. 6207430  
GENERAL INFORMATION:  
APPLICANT: Yaver, Debbie S.  
APPLICANT: Brown, Kimberley M.  
APPLICANT: Kauppinen, Sakari  
APPLICANT: Halkier, Torben P  
TITLE OF INVENTION: PURIFIED COPRINUS LACCASES AND NUCLEIC ACIDS  
TITLE OF INVENTION: ENCODING SAME  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6207430o No. 6207430disk of No. 6207430th America, Inc.  
STREET: 405 Lexington Avenue, 64th Floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/389,528  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/689,421  
FILING DATE: 9-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Harrington, James J.  
REGISTRATION NUMBER: 38,711  
REFERENCE/DOCKET NUMBER: 4554.204-WO  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3566 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(456..578, 631..696, 746..814, 869..1015,  
1069..1140, 1199..1213, 1271..1300, 1366..1563,  
1622..2149, 2213..2233, 2303..2452, 2514..2537,  
2598..2654, 2725..2776)  
US-09-389-528-32

Query Match 76.0%; Score 15.2; DB 3; Length 3566;  
Best Local Similarity 85.0%; Pred. No. 1.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAGTTAATCGAGAGTGGCT 20  
2015  
Db 2015 GCGGTTGATCGAAAGTGGCT 1996

RESULT 28

US-09-181-827A-32/c  
; Sequence 32, Application US/09181827A  
; Patent No. 6242232  
; GENERAL INFORMATION:

```

; GENERAL INFORMATION: Debbie S.
; APPLICANT: Yaver, Kimberly M.
; APPLICANT: Brown, Kimberly M.
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Halkier, Torben P.
; APPLICANT: Halkier, Torben P.
; TITLE OF INVENTION: Purified Coprinus Laccases And Nucleic
; TITLE OF INVENTION: Acids Encoding Same
; FILE REFERENCE: 4554.200-US
; CURRENT APPLICATION NUMBER: US/09/181,827A
; CURRENT FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/002,800
; PRIOR FILING DATE: 1995-08-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 3566
; TYPE: DNA
; ORGANISM: Coprinus cinereus
; US-09-181-827A-32

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Query Match	76.0%;	Score 15.2;	DB 3;	Length 3566;
Best Local Similarity	85.0%;	Pred. No. 1.3e+02;		
Matches 17: Conservative		0: Mismatches 3;	Indels 0	

Qy	1	GCAGTTAATGGAGAGTGGCT	20
Db	2015	GCAGTTAATGGAGAGTGGCT	1996

## RESULT 29

US-08-978-741-7/c  
; Sequence 7, Application US/08978741  
: Patent No. 6100076

PATENT NO. 6300078  
GENERAL INVENTOR:  
APPLICANT: yang wang, Michael W. Spellman  
TITLE OF INVENTION: O-Fucosyltransferase  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESS: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

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FILED DATE: 31  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P1041P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/325-1489  
TELEFAX: 650/952-9881

```

; INFORMATION FOR SEQ ID NO: 7:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 5009 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-978-741-7

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Query Match 76.0%; Score 15.2; DB 3; Length 5009;  
Best Local Similarity 85.0%; Pred. No. 1.4e+02;  
Matches 17: Conservative 0; Mismatches 3; Indels 0

QY 1 GCAGTTAATCGAGAGTGGCT 20  
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3344 GCAGCTAATGGAAGTGGCT 3325  
Dh

RESIST 30

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RESUL31 30
US-09-333-729A-8/c
; Sequence 8, Application US/09333729A
; Patent No. 6270987
; GENERAL INFORMATION:
; APPLICANT: Wang, Yang
; APPLICANT: Spellman, Michael W.
; TITLE OF INVENTION: O-Fucosyltransferase
; FILE REFERENCE: P1041PDI-Substitute
; CURRENT APPLICATION NUMBER: US/09/333, 729A
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: US 08/798,741
; PRIOR FILING DATE: 1997-11-26
; NUMBER OF SEQ ID NOS: 21
; SEQ ID NO 8
; LENGTH: 5009
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-333-729A-8

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Query Match 76.0%; Score 15.2; DB 3; Length 5009;  
Best Local Similarity 85.0%; Pred. No. 1.4e+02;  
Matches 17: Conservative 0: Mismatches 3: Indels 0

QY 1 GCAGTTAATGGAGAGTGGCT 20  
Dh 3344 GCAGCTAATGGAAACTGGCT 3325

## RESULT, T 31

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RESULI_31
US-09-248-796A-6732
; Sequence 6732, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO
; ACID COMPOSITIONS FOR DIAGNOSTICS AND T
; THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 6732
; LENGTH: 240
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-6732

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Query Match	75.0%;	Score 15;	DB 4;	Length 240;
Best Local Similarity	100.0%;	Pred. No. 92;		
Matches 15:	Conservative	0:	Mismatches	0:
	Indels			

3 AGTTAATGGAGAGTG 17  
Ov

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Db      171 AGTTAATGGAGAGTG 185
|||||
RESULT 32
US-09-513-999C-1833
; Sequence 1833, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 1833
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: 103...438
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: 120
; OTHER INFORMATION: s=g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 128
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 396
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 9
; OTHER INFORMATION: Xaa=Ile or Asn
US-09-513-999C-1833
Query Match      74.0%; Score 14.8; DB 4; Length 438;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 GCAGTTAATGGAGAGTGCT 20
|||||
Db      379 GCAGTGCATGGAGAGAGCT 398
|||||
RESULT 33
US-09-976-594-432
; Sequence 432, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 432
; LENGTH: 543
; TYPE: DNA
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 027185.1
US-09-976-594-432
Query Match      74.0%; Score 14.8; DB 4; Length 543;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCAGTTAATGGAGAGTGG 18
|||||
Db      160 GAAGTTACTGGAGAGTGG 177
|||||
RESULT 34
US-09-248-796A-5837
; Sequence 5837, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 5837
; LENGTH: 867
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-5837
Query Match      74.0%; Score 14.8; DB 4; Length 867;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCAGTTAATGGAGAGTGG 18
|||||
Db      597 GCAGTTGATGGAGAGTGG 614
|||||
RESULT 35
US-09-486-382B-1
; Sequence 1, Application US/09486382B
; Patent No. 6388174
; GENERAL INFORMATION:
; APPLICANT: Hokko Chemical Industry Co., Ltd.
; APPLICANT: MINISTRY OF AGRICULTURE, FORESTRY AND FISHERIES
; TITLE OF INVENTION: Genes for encoding alpha-subunits of anthranilate
; TITLE OF INVENTION: synthase of rice, and DNAs related to said genes
; FILE REFERENCE: 10647
; CURRENT APPLICATION NUMBER: US/09/486,382B
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: JP 9-235049
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1734)
US-09-486-382B-1
Query Match      74.0%; Score 14.8; DB 3; Length 1734;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGATGCG 19  
Db 1322 CAGTTACTGGAGAGTTGC 1339

RESULT 36  
US-09-486-382B-12  
; Sequence 12, Application US/09486382B  
; Patent No. 6388174  
; GENERAL INFORMATION:  
; APPLICANT: Hokko Chemical Industry Co., Ltd.  
; APPLICANT: MINISTRY OF AGRICULTURE, FORESTRY AND FISHERIES  
; TITLE OF INVENTION: Genes for encoding alpha-subunits of anthranilate  
; TITLE OF INVENTION: synthase of rice, and DNAs related to said genes  
; FILE REFERENCE: 10647  
; CURRENT APPLICATION NUMBER: US/09/486,382B  
; CURRENT FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: JP 9-235049  
; PRIOR FILING DATE: 1997-08-29  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 1734  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Modified DNA sequence of Sequence No. 63881741  
; Patent No. 6388174  
; NAME/KEY: CDS  
; LOCATION: (1)...(1734)  
US-09-486-382B-12

Query Match 74.0%; Score 14.8; DB 3; Length 1734;  
Best Local Similarity 88.9%; Pred. No. 1.8e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 CAGTTAATGGAGATGCG 19  
Db 1322 CAGTTACTGGAGAGTTGC 1339

RESULT 37  
US-09-134-000C-1851  
; Sequence 1851, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1851  
; LENGTH: 1815  
; TYPE: DNA  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-1851

Query Match 74.0%; Score 14.8; DB 4; Length 1815;  
Best Local Similarity 88.9%; Pred. No. 1.8e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 CAGTTAATGGAGATGCG 19  
Db 619 CAGTTAATGGAAAGTGC 636

RESULT 38  
US-09-352-990-9  
; Sequence 9, Application US/09352990  
; Patent No. 6255090  
; GENERAL INFORMATION:  
; APPLICANT: Farnodu, Layo O.  
; APPLICANT: Orozco, Buddy  
; APPLICANT: Rafalski, Antoni  
; TITLE OF INVENTION: Plant Aminoacyl-tRNA Synthetase  
; FILE REFERENCE: BB-1191  
; CURRENT APPLICATION NUMBER: US/09/352,990  
; CURRENT FILING DATE: 1999-07-14  
; EARLIER APPLICATION NUMBER: 60/092,866  
; EARLIER FILING DATE: July 15, 1998  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 9  
; LENGTH: 2085  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-352-990-9

Query Match 74.0%; Score 14.8; DB 3; Length 2085;  
Best Local Similarity 88.9%; Pred. No. 1.9e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 CAGTTAATGGAGATGCG 19  
Db 665 CAGATAATGGAGATGCG 682

RESULT 39  
US-08-449-645A-10  
; Sequence 10, Application US/08449645A  
; Patent No. 5981245  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Gary M.  
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
; TITLE OF INVENTION: Kinases  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Patent Operations/RBW  
; STREET: 1840 Behavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/449,645A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-287  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2962 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..2913  
US-08-449-645A-10

Query Match 74.0%; Score 14.8; DB 2; Length 2962;  
Best Local Similarity 88.9%; Pred. No. 2e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGTTAATGGAGATGGCT 20  
|||||  
Db 2051 AGTTCATGGAGATGGCT 2068

RESULT 40  
US-08-702-367A-10  
; Sequence 10, Application US/08702367A  
; Patent No. 5981246  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Gary M.  
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
; TITLE OF INVENTION: Kinases  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Patent Operations/RW  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/702.367A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-287  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2962 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..2913  
US-08-702-367A-10

Query Match 74.0%; Score 14.8; DB 2; Length 2962;  
Best Local Similarity 88.9%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGTTAATGGAGATGGCT 20  
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Db 2051 AGTTCATGGAGATGGCT 2068

RESULT 41  
PCT-US95-04681-10  
; Sequence 10, Application PC/TUS9504681  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Gary M.  
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
; TITLE OF INVENTION: Kinases  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Patent Operations/RW  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04681  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-287  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2962 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..2913  
PCT-US95-04681-10

Query Match 74.0%; Score 14.8; DB 5; Length 2962;  
Best Local Similarity 88.9%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGTTAATGGAGATGGCT 20  
|||||  
Db 2051 AGTTCATGGAGATGGCT 2068

RESULT 42  
US-09-166-350-23  
; Sequence 23, Application US/09166350A  
; Patent No. 6440663  
; GENERAL INFORMATION:  
; APPLICANT: Scanlan, Matthew  
; APPLICANT: Chen, Yao  
; APPLICANT: Stockert, Elisabeth  
; APPLICANT: Old, Lloyd  
; APPLICANT: Jager, Elke  
; APPLICANT: Knuth, Alex  
; TITLE OF INVENTION: Renal Cancer Associated Antigens and  
; TITLE OF INVENTION: Uses Therefor  
; FILE REFERENCE: L0461/7051  
; CURRENT APPLICATION NUMBER: US/09/166.350A  
; CURRENT FILING DATE: 1998-10-05  
; EARLIER APPLICATION NUMBER: US/09/166.350  
; EARLIER FILING DATE: 1998-10-05  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 23  
; LENGTH: 3150  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-166-350-23

Query Match 74.0%; Score 14.8; DB 4; Length 3150;  
Best Local Similarity 88.9%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGTTAATGGAGATGGCT 20  
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Db 2108 AGTTCATGGAGATGGCT 2125

RESULT 43  
US-08-727-118-1/c  
; Sequence 1, Application US/08727118  
; Patent No. 5928940  
; GENERAL INFORMATION:  
; APPLICANT: MIYAZONO, KOHEI  
; APPLICANT: SAMPATH, KUBER T.